

# SEARCH REQUEST FORM

Access DB#

Scientific and Technical Information Center

60447

Requester's Full Name: R GITOMER Examiner #: 69630 Date: 2/14/02  
 Art Unit: 1623 Phone Number 30 8-0732 Serial Number: 09/876,091  
 Mail Box and Bldg/Room Location: 8B19 Results Format Preferred (circle): PAPER DISK E-MAIL  
7A11

If more than one search is submitted, please prioritize searches in order of need. MEJ  
 \*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_  
 Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

JAN

RECEIVED  
 FEB 15 2002  
 (STIC)

Jan Delaval  
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 CM1 1E37 - 703-308-4498  
 jan.delaval@uspto.gov

## STAFF USE ONLY

Searcher: <u>Jan</u>	Type of Search	Vendors and cost where applicable
Searcher Phone #: <u>4498</u>	NA Sequence (#) _____	STN <input checked="" type="checkbox"/>
Searcher Location: _____	AA Sequence (#) <u>5</u>	Dialog _____
Date Searcher Picked Up: <u>2/24/02</u>	Structure (#) _____	Questel/Orbit _____
Date Completed: <u>3/1/02</u>	Bibliographic <input checked="" type="checkbox"/>	Dr.Link _____
Searcher Prep & Review Time: _____	Litigation _____	Lexis/Nexis _____
Clerical Prep Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Online Time: _____	Patent Family _____	WWW/Internet _____
	Other _____	Other (specify) _____



=> fil reg

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STRUCTURE FILE UPDATES: 27 FEB 2002 HIGHEST RN 396639-34-2  
DICTIONARY FILE UPDATES: 27 FEB 2002 HIGHEST RN 396639-34-2

TSCA INFORMATION NOW CURRENT THROUGH July 7, 2001

Please note that search-term pricing does apply when  
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Calculated physical property data is now available. See HELP PROPERTIES  
for more information. See STNote 27, Searching Properties in the CAS  
Registry File, for complete details:  
<http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf>

The P indicator for Preparations was not generated for all of the  
CAS Registry Numbers that were added to the H/Z/CA/CAplus files between  
12/27/01 and 1/23/02. Use of the P indicator in online and SDI searches  
during this period, either directly appended to a CAS Registry Number  
or by qualifying an L-number with /P, may have yielded incomplete results.  
As of 1/23/02, the situation has been resolved. Also, note that searches  
conducted using the PREP role indicator were not affected.

Customers running searches and/or SDIs in the H/Z/CA/CAplus files  
incorporating CAS Registry Numbers with the P indicator between 12/27/01  
and 1/23/02, are encouraged to re-run these strategies. Contact the  
CAS Help Desk at 1-800-848-6533 in North America or 1-614-447-3698,  
worldwide, or send an e-mail to [help@cas.org](mailto:help@cas.org) for further assistance or to  
receive a credit for any duplicate searches.

=> d sta que l10

L7 109 SEA FILE=REGISTRY ABB=ON PLU=ON PLGL.{0,1}AR/SQSP  
L9 52 SEA FILE=REGISTRY ABB=ON PLU=ON L7 AND 7/SQL  
L10 4 SEA FILE=REGISTRY ABB=ON PLU=ON L9 AND OC5-C6/ES

=> d his

(FILE 'HOME' ENTERED AT 06:28:19 ON 01 MAR 2002)  
SET COST OFF

FILE 'REGISTRY' ENTERED AT 06:29:12 ON 01 MAR 2002  
E PLGLAR/SQEP

FILE 'HCAPLUS' ENTERED AT 06:29:28 ON 01 MAR 2002  
E DE2000-10028204/AP,PRN

L1 1 S E3,E4  
E WEITHMANN K/AU  
L2 55 S E4-E7,E9  
E WEITHMAN K/AU  
L3 560 S (AVENTIS(L)PHARM?)/PA,CS  
L4 1142 S AVENTIS/PA,CS  
SEL RN L1

FILE 'REGISTRY' ENTERED AT 06:31:15 ON 01 MAR 2002

L5 7 S E1-E7  
L6 1 S L5 AND SQL/FA  
E PLGL/SQEP  
L7 109 S PLGL.{0,1}AR/SQSP  
L8 0 S L7 AND 6/SQL



L9 52 S L7 AND 7/SQL  
 L10 4 S L9 AND OC5-C6/ES  
 L11 4 S L6,L10  
 L12 1 S COLLAGENASE/CN

FILE 'HCAOLD' ENTERED AT 06:35:23 ON 01 MAR 2002

L13 0 S L11

FILE 'HCAPLUS' ENTERED AT 06:35:28 ON 01 MAR 2002

L14 12 S L11  
 L15 14517 S L12 OR COLLAGENASE  
 L16 69990 S COLLAGEN  
 E COLLAGEN/CT  
 E E3\_ALL  
 E COLLAGEN/CT  
 E E3+ALL  
 L17 2132 S E1  
 E E2+ALL  
 L18 54861 S E3+NT  
 L19 5 S L14 AND L15  
 L20 4 S L14 AND L16-L18  
 L21 6 S L19,L20

FILE 'REGISTRY' ENTERED AT 06:36:40 ON 01 MAR 2002

L22 205 S ?COLLAGENASE?/CNS

FILE 'HCAPLUS' ENTERED AT 06:36:49 ON 01 MAR 2002

L23 10136 S L22  
 L24 6 S L23 AND L14  
 L25 7 S L21,L24  
 L26 4 S L14 AND ?COLLAGENASE?  
 L27 7 S L25,L26  
 L28 1 S L14,L27 AND L2-L4  
 L29 37863 S PROTEIN#/CW (L) (ANST OR ANT OR ARG OR CAT)/RL  
 L30 1 S L14 AND L29  
 L31 12 S L14,L27,L28,L30  
 L32 10 S L31 AND (SCREEN? OR TEST? OR LIGAND OR INHIBIT?)  
 L33 12 S L31,L32  
 L34 12 S L33 AND SUBSTRATE

FILE 'USPATFULL, USPAT2' ENTERED AT 06:40:20 ON 01 MAR 2002

L35 0 S L11

FILE 'BIOSIS' ENTERED AT 06:40:25 ON 01 MAR 2002

L36 0 S L11

FILE 'REGISTRY' ENTERED AT 06:40:50 ON 01 MAR 2002

=> d l11 sqide can tot

L11 ANSWER 1 OF 4 REGISTRY COPYRIGHT 2002 ACS  
 RN 210816-75-4 REGISTRY  
 CN L-Argininamide, 1-[(7-methoxy-2-oxo-2H-1-benzopyran-3-yl)acetyl]-L-prolyl-  
 L-leucylglycyl-L-leucyl-3-[(2,4-dinitrophenyl)amino]-L-alanyl-L-alanyl-,  
 monoacetate (9CI) (CA INDEX NAME)  
 FS PROTEIN SEQUENCE; STEREOSEARCH  
 SQL 7  
 NTE modified

type	location	description
terminal mod.	Arg-7	C-terminal amide
uncommon	Dpr-5	-
modification	-	undetermined modification
modification	Pro-1	undetermined modification
modification	Dpr-5	2,4-dinitrophenyl<DNP>



SEQ 1 PLGLXAR

=====

HITS AT: 1-7

MF C49 H68 N14 O15 . C2 H4 O2

SR CAS Registry Services

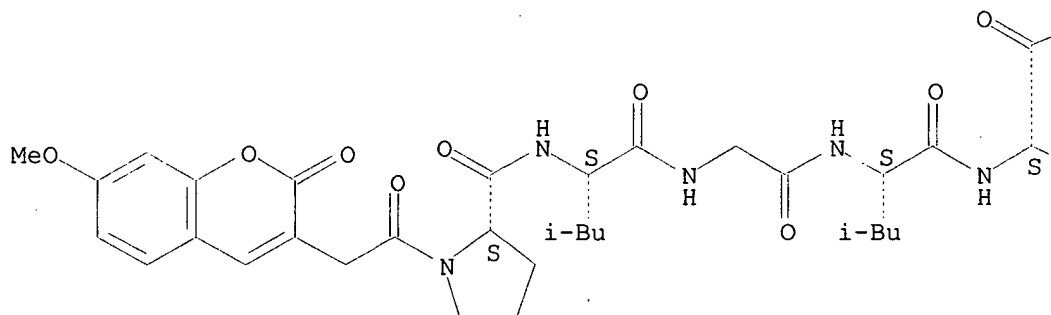
CM 1

CRN 210816-74-3

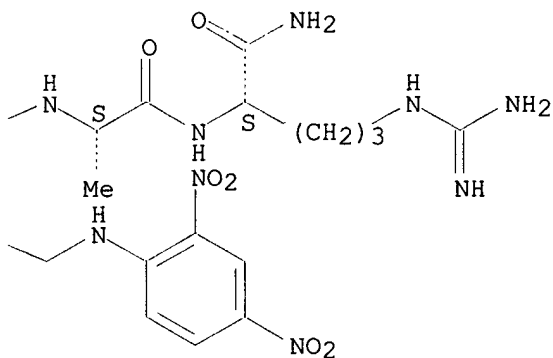
CMF C49 H68 N14 O15

Absolute stereochemistry.

PAGE 1-A



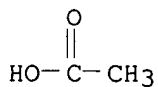
PAGE 1-B



CM 2

CRN 64-19-7

CMF C2 H4 O2







RN 210816-74-3 REGISTRY  
 CN L-Argininamide, 1-[(7-methoxy-2-oxo-2H-1-benzopyran-3-yl)acetyl]-L-prolyl-L-leucylglycyl-L-leucyl-3-[(2,4-dinitrophenyl)amino]-L-alanyl-L-alanyl-(9CI) (CA INDEX NAME)  
 FS PROTEIN SEQUENCE; STEREOSEARCH  
 SQL 7  
 NTE modified

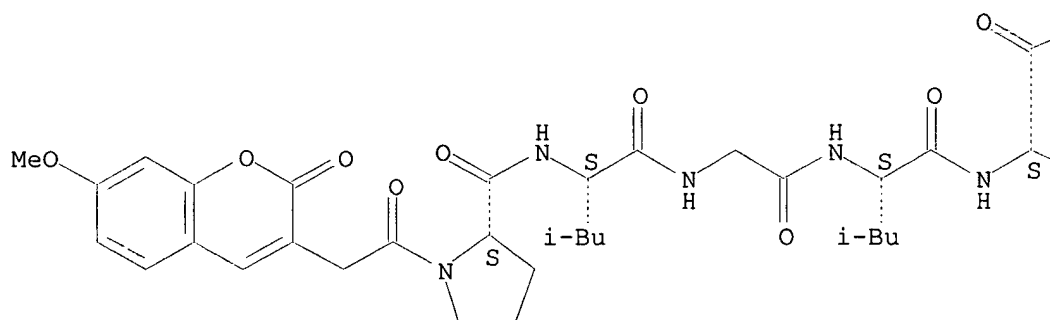
type	location		description
terminal mod.	Arg-7	-	C-terminal amide
uncommon	Dpr-5	-	-
modification	Pro-1	-	undetermined modification
modification	Dpr-5	-	2,4-dinitrophenyl<DNP>

SEQ 1 PLGLXAR

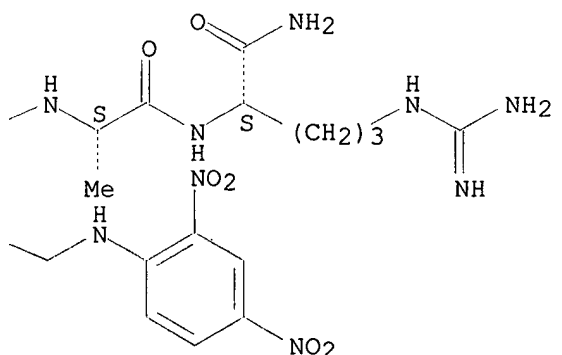
HITS AT: 1-7  
 MF C49 H68 N14 O15  
 CI COM  
 SR CAS Registry Services  
 LC STN Files: CA, CAPLUS, TOXCENTER

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



1 REFERENCES IN FILE CA (1967 TO DATE)  
 1 REFERENCES IN FILE CAPLUS (1967 TO DATE)



REFERENCE 1: 136:50643

L11 ANSWER 3 OF 4 REGISTRY COPYRIGHT 2002 ACS

RN 182929-39-1 REGISTRY

CN L-Argininamide, 1-[(2-oxo-2H-1-benzopyran-4-yl)acetyl]-L-prolyl-L-leucylglycyl-L-leucyl-3-[(2,4-dinitrophenyl)amino]-L-alanyl-L-alanyl-(9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE; STEREOSEARCH

SQL 7

NTE modified

type	----- location -----	description
terminal mod.	Arg-7 -	C-terminal amide.
uncommon	Dpr-5 -	-
modification	Pro-1 -	undetermined modification
modification	Dpr-5 -	2,4-dinitrophenyl<DNP>

SEQ 1 PLGLXAR

=====

HITS AT: 1-7

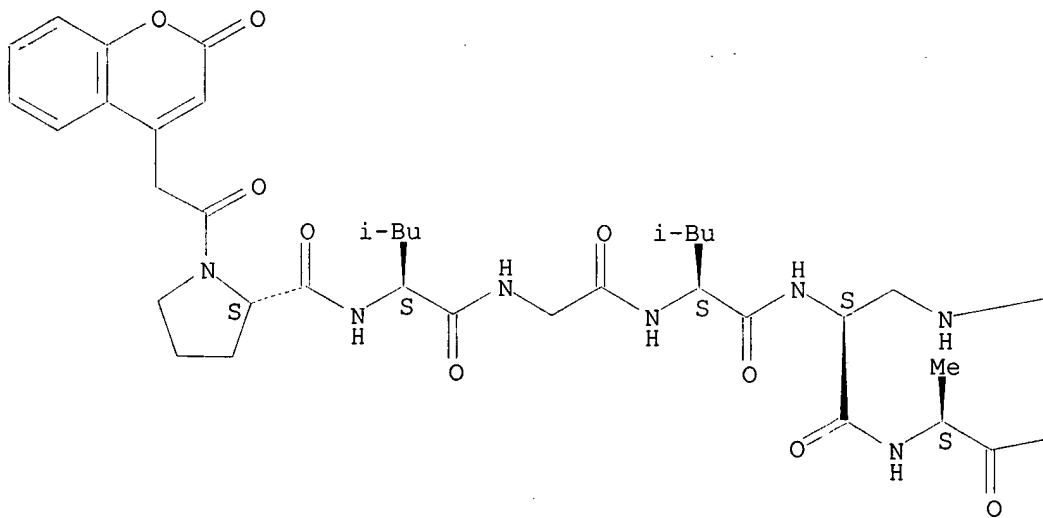
MF C48 H66 N14 O14

SR CA

LC STN Files: CA, CAPLUS

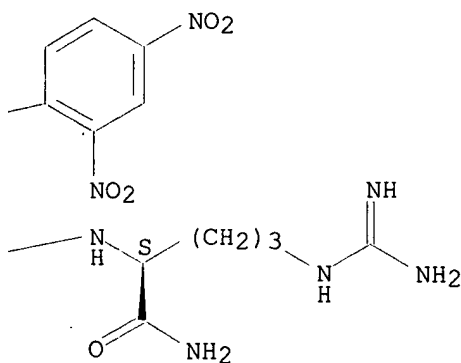
Absolute stereochemistry.

PAGE 1-A





PAGE 1-B



1 REFERENCES IN FILE CA (1967 TO DATE)

1 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 125:295954

L11 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2002 ACS

RN 140430-53-1 REGISTRY

CN L-Argininamide, 1-[(7-methoxy-2-oxo-2H-1-benzopyran-4-yl)acetyl]-L-prolyl-L-leucylglycyl-L-leucyl-3-[(2,4-dinitrophenyl)amino]-L-alanyl-L-alanyl-(9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE; STEREOSEARCH

SQL 7

NTE modified

type	----- location -----	description
terminal mod.	Arg-7	C-terminal amide
uncommon	Dpr-5	-
modification	Pro-1	undetermined modification
modification	Dpr-5	2,4-dinitrophenyl<DNP>

SEQ 1 PLGLXAR

=====

HITS AT: 1-7

MF C49 H68 N14 O15

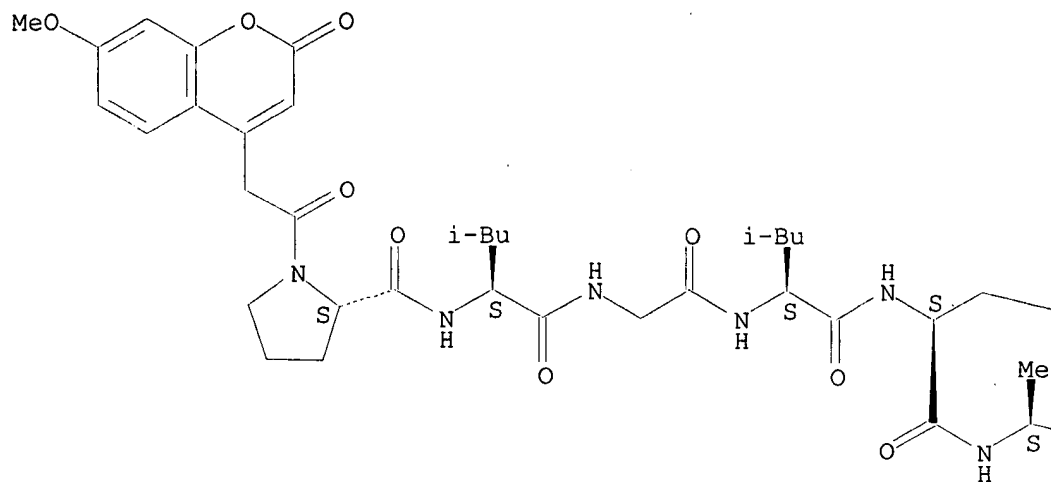
SR CA

LC STN Files: CA, CAPLUS, CHEMCATS, TOXCENTER

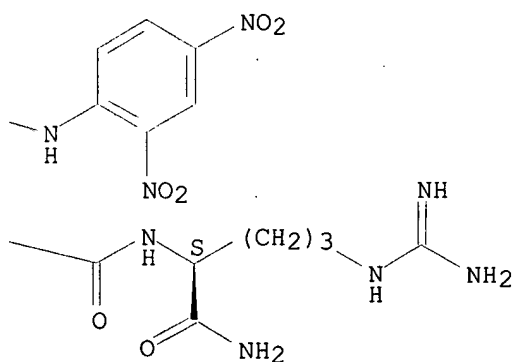
Absolute stereochemistry.



PAGE 1-A



PAGE 1-B



10 REFERENCES IN FILE CA (1967 TO DATE)  
 10 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 135:15967  
 REFERENCE 2: 134:174724  
 REFERENCE 3: 132:119120  
 REFERENCE 4: 132:46928  
 REFERENCE 5: 131:348235  
 REFERENCE 6: 127:187274  
 REFERENCE 7: 127:118829  
 REFERENCE 8: 122:208637





REFERENCE 9: 117:43338

REFERENCE 10: 116:230498

=> d 112 ide can

L12 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2002 ACS

RN 9001-12-1 REGISTRY

CN **Collagenase (9CI)** (CA INDEX NAME)

OTHER NAMES:

CN Aspergillopeptidase C

CN Azocollase

CN Clostridiopeptidase A

CN Clostridiopeptidase I

CN Clostridiopeptidase II

CN Collagen peptidase

CN Collagen protease

CN Collagenase A

CN Collagenase MMP-1

CN E.C. 3.4.24.3

CN E.C. 3.4.24.34

CN E.C. 3.4.24.7

CN E.C. 3.4.4.19

CN E.C. 3.4.99.5

CN Interstitial collagenase

CN Kollaza

CN Matrix metalloproteinase-1

CN Matrix metalloproteinase-18

CN Matrix metalloproteinase-8

CN Metallocollagenase

CN Metalloproteinase-1

CN MMP-1

CN MMP-8

CN Morikraz

CN Nucleolysin

CN Peptidase, clostridio-, A

CN Proteinase, Clostridium histolyticum, A

CN Soycollagestin

DR 37288-86-1, 39433-96-0

MF Unspecified

CI COM, MAN

LC STN Files: ADISNEWS, AGRICOLA, ANABSTR, BIOBUSINESS, BIOSIS, BIOTECHNO,  
CA, CABA, CAPLUS, CASREACT, CBNB, CEN, CHEMCATS, CHEMLIST, CIN, CSCHEM,  
DDFU, DIOGENES, DRUGU, EMBASE, IFICDB, IFIPAT, IFIUDB, IPA, MEDLINE,  
MRCK\*, MSDS-OHS, PHAR, PIRA, PROMT, TOXCENTER, TOXLIT, USPAT2, USPATFULL

(\*File contains numerically searchable property data)

Other Sources: EINECS\*\*, TSCA\*\*

(\*\*Enter CHEMLIST File for up-to-date regulatory information)

\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*

6511 REFERENCES IN FILE CA (1967 TO DATE)

69 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA

6528 REFERENCES IN FILE CAPLUS (1967 TO DATE)

REFERENCE 1: 136:134761

REFERENCE 2: 136:133595

REFERENCE 3: 136:133383

REFERENCE 4: 136:132207

REFERENCE 5: 136:130881



REFERENCE 6: 136:130844  
REFERENCE 7: 136:128574  
REFERENCE 8: 136:123405  
REFERENCE 9: 136:117317  
REFERENCE 10: 136:116447

=> fil hcaplus  
FILE 'HCAPLUS' ENTERED AT 06:41:42 ON 01 MAR 2002  
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FILE COVERS 1907 - 1 Mar 2002 VOL 136 ISS 9  
FILE LAST UPDATED: 27 Feb 2002 (20020227/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

CAS roles have been modified effective December 16, 2001. Please check your SDI profiles to see if they need to be revised. For information on CAS roles, enter HELP ROLES at an arrow prompt or use the CAS Roles thesaurus (/RL field) in this file.

The P indicator for Preparations was not generated for all of the CAS Registry Numbers that were added to the CAS files between 12/27/01 and 1/23/02. As of 1/23/02, the situation has been resolved. Searches and/or SDIs in the H/Z/CA/CAplus files incorporating CAS Registry Numbers with the P indicator executed between 12/27/01 and 1/23/02 may be incomplete. See the NEWS message on this topic for more information.

=> d all tot 134

L34 ANSWER 1 OF 12 HCAPLUS COPYRIGHT 2002 ACS

AN 2001:904565 HCAPLUS

DN 136:50643

TI Method for identifying medically valuable active substances

IN **Weithmann, Klaus Ulrich**

PA **Aventis Pharma** Deutschland GmbH, Germany

SO PCT Int. Appl., 14 pp.

CODEN: PIXXD2

DT Patent

LA German

IC ICM C12Q001-00

CC 9-2 (Biochemical Methods)

Section cross-reference(s): 63

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001094612	A2	20011213	WO 2001-EP6143	20010530
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,				



CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM,  
 HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,  
 LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO,  
 RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN,  
 YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM  
 RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,  
 DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,  
 BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

DE 10028204 A1 20020103 DE 2000-10028204 20000609

PRAI DE 2000-10028204 A 20000609

AB The invention relates to a method for identifying **inhibitors** or **ligands** for binding domains. The inventive method comprises using a protein that has at least one catalytic domain, incubating it with a marker **substrate** that binds to the catalytic domain of the protein and reacts therewith, with a **substrate** that can reversibly bind to the catalytic domain and to the binding domain, and with the **inhibitor**, and detecting whether the protein reacts with the marker **substrate**.

ST drug detection protein binding **inhibitor**; catalyst protein binding **inhibitor** detection drug

IT Cachexia  
 Osteoarthritis  
 (agents **inhibiting**; method for identifying medically valuable active substances)

IT Antiarteriosclerotics  
 (antiatherosclerotics; method for identifying medically valuable active substances)

IT Disease, animal  
 (chronic, agents **inhibiting**; method for identifying medically valuable active substances)

IT Cartilage  
 Connective tissue  
 Joint, anatomical  
 Periodontium  
 (disease, agents **inhibiting**; method for identifying medically valuable active substances)

IT Wound healing  
 (disorders, agents **inhibiting**; method for identifying medically valuable active substances)

IT **Proteins**  
 RL: ANT (Analyte); ANST (Analytical study)  
 (ligand-binding; method for identifying medically valuable active substances)

IT Bone  
 (metabolic disorders, agents **inhibiting**; method for identifying medically valuable active substances)

IT Antitumor agents  
 (metastasis; method for identifying medically valuable active substances)

IT Anti-inflammatory agents  
 Antiarthritics  
 Antitumor agents  
 Antiulcer agents  
 Biomarkers (biological responses)  
 Carriers  
 Drugs  
 (method for identifying medically valuable active substances)

IT Oligosaccharides, analysis  
 RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)  
 (method for identifying medically valuable active substances)

IT **Proteins**  
 RL: ARG (Analytical reagent use); CAT (Catalyst use); ANST (Analytical study); USES (Uses)  
 (method for identifying medically valuable active substances)

IT **Collagens, analysis**



RL: ARU (Analytical role, unclassified); ANST (Analytical study)  
(method for identifying medically valuable active substances)

IT Bone formation  
(mineralization, disorders, agents **inhibiting**; method for  
identifying medically valuable active substances)

IT Muscle, disease  
(myalgia, agents **inhibiting**; method for identifying medically  
valuable active substances)

IT Catalysts  
(proteins contg.; method for identifying medically valuable active  
substances)

IT Shock (circulatory collapse)  
(septic, agents **inhibiting**; method for identifying medically  
valuable active substances)

IT Spinal column  
(spondylitis, agents **inhibiting**; method for identifying  
medically valuable active substances)

IT Drugs  
(stenosis-**inhibiting**; method for identifying medically  
valuable active substances)

IT Appetite  
(stimulants; method for identifying medically valuable active  
substances)

IT Protamines  
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL  
(Biological study); USES (Uses)  
(sulfates; method for identifying medically valuable active substances)

IT Oligosaccharides, analysis  
Oligosaccharides, analysis  
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL  
(Biological study); USES (Uses)  
(tetrasaccharides; method for identifying medically valuable active  
substances)

IT **Collagens, analysis**  
RL: ARU (Analytical role, unclassified); ANST (Analytical study)  
(type II; method for identifying medically valuable active substances)

IT 564-25-0, Doxycycline 53597-25-4 81669-70-7, Metalloproteinase  
147172-61-0, Aggrecanase  
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL  
(Biological study); USES (Uses)  
(method for identifying medically valuable active substances)

IT **9001-12-1, Collagenase**  
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified);  
ANST (Analytical study); BIOL (Biological study); USES (Uses)  
(method for identifying medically valuable active substances)

IT **210816-74-3**  
RL: ARU (Analytical role, unclassified); ANST (Analytical study)  
(method for identifying medically valuable active substances)

IT 380451-86-5  
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)  
(method for identifying medically valuable active substances)

L34 ANSWER 2 OF 12 HCAPLUS COPYRIGHT 2002 ACS

AN 2001:230817 HCAPLUS

DN 135:15967

TI The role of exon 5 in fibroblast **collagenase** (MMP-1)  
**substrate** specificity and **inhibitor** selectivity

AU Knauper, Vera; Patterson, Margaret L.; Gomis-Ruth, Franz X.; Smith, Bryan;  
Lyons, Alan; Docherty, Andrew J. P.; Murphy, Gillian

CS School of Biological Sciences, University of East Anglia, Norwich, UK

SO Eur. J. Biochem. (2001), 268(6), 1888-1896

CODEN: EJBCAI; ISSN: 0014-2956

PB Blackwell Science Ltd.

DT Journal

LA English

CC 7-5 (Enzymes)





- AB Interstitial **collagen** is degraded by members of the matrix metalloproteinase (MMP) family, including MMP-1. Previous work has shown that the region of MMP-1 coded for by exon 5 is implicated both in **substrate** specificity and **inhibitor** selectivity. We have constructed a chimeric enzyme, the exon 5 chimera, consisting primarily of MMP-1, with the region coded for by exon 5 replaced with the equiv. region of MMP-3, a noncollagenolytic MMP. Unlike MMP-3, the exon 5 chimera is capable of cleaving type I **collagen**, but the activity is only 2.2% of trypsin-activated MMP-1. "Superactivation" of the chimera has no discernible effect, suggesting that the salt bridge formed in "superactive" MMP-1 is not present. The kinetics for exon 5 chimera cleavage of two synthetic **substrates** display an MMP-3 phenotype, however, cleavage of gelatin is slightly impaired as compared to the parent enzymes. The Kiapp values for the exon 5 chimera complexed with synthetic **inhibitors** and N-terminal TIMP-2 also show a more MMP-3-like behavior. However, the kon values for N-terminal TIMP-1 and N-terminal TIMP-2 are more comparable to those for MMP-1. These data show that the region of MMP-1 coded for by exon 5 is involved in both **substrate** specificity and **inhibitor** selectivity and the structural basis for our findings is discussed.
- ST **collagenase** exon **substrate** **inhibitor** specificity fibroblast
- IT Enzyme functional sites  
(active; the role of exon 5 in fibroblast **collagenase** (MMP-1) **substrate** specificity and **inhibitor** selectivity)
- IT Enzyme kinetics  
(of **inhibition**; the role of exon 5 in fibroblast **collagenase** (MMP-1) **substrate** specificity and **inhibitor** selectivity)
- IT Secondary structure  
(protein; the role of exon 5 in fibroblast **collagenase** (MMP-1) **substrate** specificity and **inhibitor** selectivity)
- IT Enzyme functional sites  
(**substrate**-binding; the role of exon 5 in fibroblast **collagenase** (MMP-1) **substrate** specificity and **inhibitor** selectivity)
- IT Enzyme kinetics  
Post-translational processing  
Protein degradation  
(the role of exon 5 in fibroblast **collagenase** (MMP-1) **substrate** specificity and **inhibitor** selectivity)
- IT **Collagens, biological studies**  
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)  
(type I; the role of exon 5 in fibroblast **collagenase** (MMP-1) **substrate** specificity and **inhibitor** selectivity)
- IT 124861-55-8, TIMP-2 145337-55-9, Ro31-9790 162514-46-7, CT 1746  
RL: BAC (Biological activity or effector, except adverse); BIOL (Biological study)  
(the role of exon 5 in fibroblast **collagenase** (MMP-1) **substrate** specificity and **inhibitor** selectivity)
- IT 9001-12-1, **Collagenase**  
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); PRP (Properties); BIOL (Biological study); PROC (Process)  
(the role of exon 5 in fibroblast **collagenase** (MMP-1) **substrate** specificity and **inhibitor** selectivity)
- IT 79955-99-0, Matrix metalloproteinase 3  
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)  
(the role of exon 5 in fibroblast **collagenase** (MMP-1) **substrate** specificity and **inhibitor** selectivity)
- IT 39287-99-5P, Pro-collagenase  
RL: BPN (Biosynthetic preparation); BPR (Biological process); BIOL (Biological study); PREP (Preparation); PROC (Process)  
(the role of exon 5 in fibroblast **collagenase** (MMP-1) **substrate** specificity and **inhibitor** selectivity)



IT 140430-53-1 256394-92-0 256394-94-2

RL: BPR (Biological process); BIOL (Biological study); PROC (Process)  
(the role of exon 5 in fibroblast **collagenase** (MMP-1)  
**substrate** specificity and **inhibitor** selectivity)

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L34 ANSWER 3 OF 12 HCAPLUS COPYRIGHT 2002 ACS

AN 2001:9504 HCAPLUS

DN 134:174724

TI Effects of dimethyl sulfoxide, temperature, and sodium chloride on the activity of human matrix metalloproteinase 7 (matrilysin)

AU Oneda, Hiroshi; Inouye, Kuniyo

CS Division of Applied Life Sciences, Graduate School of Agriculture, Kyoto University, Kyoto, 606-8502, Japan

SO J. Biochem. (Tokyo) (2000), 128(5), 785-791

CODEN: JOBIAO; ISSN: 0021-924X

PB Japanese Biochemical Society

DT Journal

LA English

CC 7-3 (Enzymes)

AB Effects of DMSO (DMSO), temp., and sodium chloride on the matrilysin-catalyzed hydrolysis of (7-methoxycoumarin-4-yl)acetyl-L-Pro-L-Leu-Gly-L-Leu-[N3-(2,4- dinitrophenyl)-L-2,3-diamino-propionyl]-L-Ala-L-Arg-NH2 [MOCac-PLGL(Dpa)AR] were examd. DMSO **inhibited** the matrilysin activity competitively with the **inhibitor** const. (Ki) of 0.59+-0.04 M, and the binding between them was endothermic and entropy-driven. The binding of matrilysin with MOCac-PLGL(Dpa)AR was also



found to be entropy-driven. The matrilysin activity was increased in a biphasic exponential fashion with increasing concn. of NaCl, and was 5.3 times higher in the presence of 4 M NaCl than that in its absence. The first and second phases were sepd. at 0.5 M NaCl, and the activation at x M NaCl compared with the activity in the absence of NaCl was expressed as 2.1x at [NaCl] < 0.5 M and 1.4x at [NaCl] > 0.5 M. The activation was brought about solely through a decrease in the Michaelis const. (Km), and the catalytic const. (kcat) was not much altered. This suggests that the decrease in the electrostatic interaction and the increase in the hydrophobic interaction between matrilysin and the **substrate** might enhance the enzyme activity by reducing the Km value.

- ST matrilysin dimethyl sulfoxide temp sodium chloride; matrix metalloproteinase DMSO temp salt
- IT Michaelis constant  
(effects of DMSO, temp., and sodium chloride on activity of human matrix metalloproteinase 7 (matrilysin))
- IT Enzyme kinetics  
(of **inhibition**; effects of DMSO, temp., and sodium chloride on activity of human matrix metalloproteinase 7 (matrilysin))
- IT 67-68-5, Dimethyl sulfoxide, biological studies 7647-14-5, Sodium chloride, biological studies  
RL: BAC (Biological activity or effector, except adverse); BIOL (Biological study)  
(effects of DMSO, temp., and sodium chloride on activity of human matrix metalloproteinase 7 (matrilysin))
- IT 141256-52-2, Matrilysin  
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BIOL (Biological study); PROC (Process)  
(effects of DMSO, temp., and sodium chloride on activity of human matrix metalloproteinase 7 (matrilysin))
- IT 140430-53-1  
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)  
(effects of DMSO, temp., and sodium chloride on activity of human matrix metalloproteinase 7 (matrilysin))

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- L34 ANSWER 4 OF 12 HCAPLUS COPYRIGHT 2002 ACS  
 AN 1999:798816 HCAPLUS  
 DN 132:119120  
 TI Matrix metalloproteinase homologues from Arabidopsis thaliana. Expression and activity  
 AU Maidment, Jill M.; Moore, Darren; Murphy, George P.; Murphy, Gillian; Clark, Ian M.  
 CS School of Biological Sciences, University of East Anglia, Norwich, NR4 7TJ, UK  
 SO J. Biol. Chem. (1999), 274(49), 34706-34710  
 CODEN: JBCHA3; ISSN: 0021-9258  
 PB American Society for Biochemistry and Molecular Biology  
 DT Journal  
 LA English  
 CC 7-2 (Enzymes)  
 Section cross-reference(s): 11
- AB Five genes potentially encoding novel matrix metalloproteinases (MMPs) have been identified on the Arabidopsis thaliana data base. The predicted proteins have a similar domain structure to mammalian MMP-7, with a propeptide and catalytic domain but no C-terminal hemopexin-like domain. Four of the A. thaliana MMPs (At-MMPs) have a predicted C-terminal transmembrane domain. The At-MMPs are differentially expressed in flower, leaf, root, and stem tissues from 14-day-old plants. The cDNA for one of the At-MMPs (At1-MMP) was cloned and expressed in Escherichia coli. Following refolding and purifn., the proenzyme At1-MMP was shown to undergo autolytic activation in the presence of an organomercurial with a concomitant decrease in Mr. In contrast to this, trypsin-treatment led to the formation of an inactive product. The activated At1-MMP digested myelin basic protein, but was unable to digest gelatin or casein. Three peptide **substrates** for MMPs were also cleaved by At1-MMP. The enzyme activity of At1-MMP was **inhibited** by human tissue **inhibitors** of metalloproteinases 1 and 2 and the hydroxamate **inhibitor** BB-94.
- ST Arabidopsis matrix metalloproteinase gene expression; At1 matrix metalloproteinase processing Arabidopsis
- IT Flower  
 Leaf  
 Post-translational processing  
 Root  
 Stem  
 (expression of At1-At5 matrix metalloproteinase homologs from Arabidopsis thaliana and cloning and activity of At1 matrix metalloproteinase)
- IT Myelin basic protein  
 RL: BPR (Biological process); BIOL (Biological study); PROC (Process)  
 (expression of At1-At5 matrix metalloproteinase homologs from Arabidopsis thaliana and cloning and activity of At1 matrix metalloproteinase)
- IT Gene, plant  
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)  
 (for matrix metalloproteinase homologs; expression of At1-At5 matrix metalloproteinase homologs from Arabidopsis thaliana and cloning and activity of At1 matrix metalloproteinase)
- IT Protein sequences  
 (homol.; expression of At1-At5 matrix metalloproteinase homologs from Arabidopsis thaliana and cloning and activity of At1 matrix metalloproteinase)
- IT 141907-41-7P, Matrix metalloproteinase  
 RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); PUR (Purification or recovery); BIOL (Biological study); PREP (Preparation);





## PROC (Process)

(expression of At1-At5 matrix metalloproteinase homologs from Arabidopsis thaliana and cloning and activity of At1 matrix metalloproteinase)

IT 140430-53-1 256394-92-0 256394-94-2

RL: BPR (Biological process); BIOL (Biological study); PROC (Process)

(expression of At1-At5 matrix metalloproteinase homologs from Arabidopsis thaliana and cloning and activity of At1 matrix metalloproteinase)

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L34 ANSWER 5 OF 12 HCAPLUS COPYRIGHT 2002 ACS

AN 1999:674594 HCAPLUS

DN 132:46928

TI Biochemical characterization of the catalytic domain of membrane-type 4 matrix metalloproteinase

AU Kolkenbrock, Hansjorg; Essers, Lutz; Ulbrich, Norbert; Will, Horst

CS Deutsches Rheumaforschungszentrum Berlin, Berlin, D-10117, Germany

SO Biol. Chem. (1999), 380(9), 1103-1108

CODEN: BICHF3; ISSN: 1431-6730

PB Walter de Gruyter GmbH & Co. KG

DT Journal

LA English

CC 7-5 (Enzymes)

AB A C-terminal truncated form of membrane-type 4 matrix metalloproteinase (MT4-MMP; MMP 17), lacking the hemopexin-like and transmembrane domain, was expressed in Escherichia coli. The catalytic domain was produced by tryptic activation of the recombinant proenzyme and proved to be catalytically active towards the fluorogenic **substrate** for matrix metalloproteinases (7-methoxycoumarin-4-yl) acetyl-Pro-Leu-Gly-Leu(3-(2,4-dinitrophenyl)-L-2,3-diaminopropionyl)-Ala-Arg-NH<sub>2</sub>. In contrast to the other 3 MT-MMPs (MT1-, MT2-, and MT3-MMP), the catalytic domain of MT4-MMP does not activate progelatinase A, nor does it hydrolyze one of the offered extracellular matrix (ECM) proteins, such as **collagen** types I, II, III, IV, and V, gelatin, fibronectin, laminin, or decorin. TIMP-1, a poor **inhibitor** of MT1-, MT2-, and MT3-MMP, suppresses MT4-MMP activity effectively. The progelatinase A/TIMP-2 complex that usually reacts like TIMP-2 also **inhibits** MT4-MMP. TIMP-2, a strong **inhibitor** of other MT-MMPs, **inhibits** MT4-MMP at low concns. With increasing TIMP-2 concn., however, activity passes through a min. and then increases until at high TIMP-2 concn. the activity is the same as in the absence of TIMP-2. TIMP-1 or the progelatinase A/TIMP-2 complex do not prevent reactivation of MT4-MMP catalytic domain at high TIMP-2 concns.

ST catalytic domain membrane type 4 matrix metalloproteinase; MT4MMP

catalytic domain **inhibition** homol

IT Protein motifs

(catalytic domain of membrane-type 4 matrix metalloproteinase, biochem. characterization)



IT 203810-08-6, MT4-MMP  
RL: BPR (Biological process); PRP (Properties); BIOL (Biological study);  
PROC (Process)  
(catalytic domain of membrane-type 4 matrix metalloproteinase, biochem.  
characterization)

IT 124861-55-8, TIMP-2 140208-24-8, TIMP-1  
RL: BAC (Biological activity or effector, except adverse); BIOL  
(Biological study)  
(catalytic domain of membrane-type 4 matrix metalloproteinase,  
**inhibition**)

IT 140430-53-1  
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)  
(catalytic domain of membrane-type 4 matrix metalloproteinase,  
**substrate** specificity)

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L34 ANSWER 6 OF 12 HCAPLUS COPYRIGHT 2002 ACS

AN 1999:525936 HCAPLUS

DN 131:348235

TI Purification and partial characterization of a soluble metallopeptidase  
from *Xenopus* oocytes

AU Okida, Noriyuki; Tokumoto, Toshinobu; Ishikawa, Katsutoshi

CS Department of Biology and Geosciences, Faculty of Science, Shizuoka  
University, Shizuoka, 422-8529, Japan

SO J. Biochem., Mol. Biol. Biophys. (1999), 3(1), 1-8  
CODEN: JBMBF6; ISSN: 1025-8140

PB Harwood Academic Publishers

DT Journal

LA English

CC 7-2 (Enzymes)

AB A new peptidase, which we call metallopeptidase, was purified from the



cytosol of *Xenopus* oocytes. The enzyme cleaved the Gly-Leu bond in (7-methoxy-coumarin-4-yl) acetyl-L-Prolyl-L-Leucyl-Glycyl-L-Leucyl-[N3-(2,4-dinitrophenyl)-L-2,3-diaminopropionyl]-L-Alanyl-L-Arginine amide (MOCac-Pro-Leu-Gly-Leu-A2pr(Dnp)-Ala-Arg-NH<sub>2</sub>) as a fluorogenic **substrate** for the matrix metallopeptidase. Its apparent mol. mass was estd. to be 76 kDa by SDS-PAGE. The activity was markedly **inhibited** by metal-chelating agents such as o-phenanthroline and EDTA. However, o-phenanthroline-**inhibited** enzyme was significantly reactivated on addn. of Zn<sup>2+</sup>. Thus, this zinc-contg. enzyme must be an intracellular metallopeptidase. The optimal pH for enzyme activity at 37.degree.C was found to be neutral and slightly alk., indicating that the enzyme was derived from a non-lysosomal location. The optimal temp. was 50.degree.C at pH 7.5 and the enzyme was stable below 30.degree.C. This enzyme may be a new target for Zn<sup>2+</sup> in the proteolytic pathway in the process of *Xenopus* oocyte maturation induced by progesterone.

ST metallopeptidase oocyte *Xenopus*

IT Egg

(oocyte; purifn. and partial characterization of a sol. metallopeptidase from *Xenopus* oocytes)

IT *Xenopus laevis*

(purifn. and partial characterization of a sol. metallopeptidase from *Xenopus* oocytes)

IT 9031-94-1P, Aminopeptidase

RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BPR (Biological process); PRP (Properties); PUR (Purification or recovery); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); PROC (Process)

(purifn. and partial characterization of a sol. metallopeptidase from *Xenopus* oocytes)

IT 7440-66-6, Zinc, biological studies 140430-53-1

RL: BPR (Biological process); BIOL (Biological study); PROC (Process) (purifn. and partial characterization of a sol. metallopeptidase from *Xenopus* oocytes)

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L34 ANSWER 7 OF 12 HCAPLUS COPYRIGHT 2002 ACS

AN 1997:444814 HCAPLUS

DN 127:187274

TI Flow injection analysis for measurement of activity of matrix metalloproteinase-7 (MMP-7)

AU Itoh, Michiyasu; Osaki, Mamoru; Chiba, Tadashige; Masuda, Kazuto; Akizawa, Toshifumi; Yoshioka, Masanori; Seiki, Motoharu

CS Department of Analytical Chemistry, Faculty of Pharmaceutical Sciences, Setsunan University, Hirakata, 573-01, Japan

SO J. Pharm. Biomed. Anal. (1997), 15(9,10), 1417-1426



CODEN: JPBADA; ISSN: 0731-7085

- PB Elsevier  
DT Journal  
LA English  
CC 7-1 (Enzymes)  
AB A simple and convenient method for measuring the activity of a recombinant human matrix metalloproteinase 7 (MMP-7, matrilysin) was developed by flow injection anal. (FIA). For this method, purified recombinant MMP-7 zymogen expressed in *E. coli* and the **substrate** peptide (MOCac-Pro-Leu-Gly-Leu-A2pr(DNP)-Ala-Arg-NH2) were used. Following the incubation of **substrate** peptide with activated r-proMMP-7, the resulting fluorescent product peptide (MOCac-Pro-Leu-Gly) was monitored with a fluorescence detector (.lambda.ex 328 nm, .lambda.em 393 nm) without chromatog. sepn. In this FIA system, the anal. time is 2 min and the std. curve is linear from 5 to 100 pmol of the product peptide injected. In order to use this FIA system as a method for **screening inhibitors** against MMP-7, the effects of CaCl2, EDTA and of the tissue **inhibitor** of metalloproteinase-1, and -2, were **tested**. A synthetic PRCGXPd-contg. peptide (BS-10) was also obsd. to **inhibit** MMP-7 activity, with an IC50 value of 104 .mu.M. Thus, it was concluded that the activity of r-MMP-7 can be reliably measured by the proposed system. Furthermore, to confirm the utility of this FIA system as a **screening** method, the **inhibitory** activity of the MMP-related substance in Joro spider (*Nephila clavata*) venom was measured by this method. This **inhibitory** activity was obsd. in an ext. of a venom dild. 1000-fold. Thus, the FIA method is not only simple and quick, but also sensitive enough to **screen** and analyze the **inhibitory** properties of a large no. of **test** compds.
- ST matrix metalloproteinase 7 flow injection analysis; matrilysin detn  
**inhibitor screening** FIA system
- IT Venoms  
(Joro spider venom MMP-related **inhibitor**; fluorogenic **substrate** peptide and flow injection anal. for measurement of matrix metalloproteinase-7 activity and **inhibitor screening**)
- IT Flow injection analysis  
(fluorogenic **substrate** peptide and flow injection anal. for measurement of matrix metalloproteinase-7 activity and **inhibitor screening**)
- IT *Nephila clavata*  
(venom MMP-related **inhibitor**; fluorogenic **substrate** peptide and flow injection anal. for measurement of matrix metalloproteinase-7 activity and **inhibitor screening**)
- IT 194234-74-7  
RL: ANT (Analyte); BAC (Biological activity or effector, except adverse); ANST (Analytical study); BIOL (Biological study)  
(BS-10, **inhibitor**, **screening inhibitors** with FIA system; fluorogenic **substrate** peptide and flow injection anal. for measurement of matrix metalloproteinase-7 activity and **inhibitor screening**)
- IT 141256-52-2, Matrix metalloproteinase 7  
RL: ANT (Analyte); BPR (Biological process); ANST (Analytical study); BIOL (Biological study); PROC (Process)  
(fluorogenic **substrate** peptide and flow injection anal. for measurement of matrix metalloproteinase-7 activity and **inhibitor screening**)
- IT 140430-53-1  
RL: ARG (Analytical reagent use); BPR (Biological process); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PROC (Process); USES (Uses)  
(fluorogenic **substrate** peptide; fluorogenic **substrate** peptide and flow injection anal. for measurement of matrix metalloproteinase-7 activity and **inhibitor screening**)





- IT 60-00-4, EDTA, biological studies 10043-52-4, Calcium chloride (CaCl<sub>2</sub>), biological studies 124861-55-8 140208-24-8, Tissue **inhibitor** of metalloproteinase-1  
RL: ANT (Analyte); BAC (Biological activity or effector, except adverse); ANST (Analytical study); BIOL (Biological study)  
(**inhibitor, screening inhibitors** with FIA system; fluorogenic **substrate** peptide and flow injection anal. for measurement of matrix metalloproteinase-7 activity and **inhibitor screening**)
- L34 ANSWER 8 OF 12 HCAPLUS COPYRIGHT 2002 ACS  
AN 1997:390011 HCAPLUS  
DN 127:118829  
TI Comparison of snake venom reprolysin and matrix metalloproteinases as models of TNF-.alpha. converting enzyme  
AU Van Dyk, Drew E.; Marchand, Petra; Bruckner, Robert C.; Fox, Jay W.; Jaffee, Bruce D.; Gunyuzlu, Paul L.; Davis, Gary L.; Nurnberg, Sherrill; Covington, Maryanne; Decicco, Carl P.; Trzaskos, James M.; Magolda, Ronald L.; Copeland, Robert A.  
CS Inflammatory Dis. Res. Chem. Phys. Sci., The DuPont Merck Res. Lab., Wilmington, DE, 19880-0400, USA  
SO Bioorg. Med. Chem. Lett. (1997), 7(10), 1219-1224  
CODEN: BMCLE8; ISSN: 0960-894X  
PB Elsevier  
DT Journal  
LA English  
CC 7-2 (Enzymes)  
AB The reprolysin ht-d was compared to several human MMPs for the ability to cleave a peptide **substrate** representing the processing site of human pro-TNF. The rank order of **inhibitor** potency for a series of hydroxamic acids was also compared among these enzymes and for **inhibition** of TNF release from human white blood cells. The results suggest that ht-d is a better model TNF-.alpha. convertase (TACE) than are the human MMPs.  
ST reprolysin matrix metalloproteinase model TNF convertase; tumor necrosis factor converting enzyme model  
IT Hemorrhagins  
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BIOL (Biological study); PROC (Process)  
(ht-d; comparison of snake venom reprolysin and matrix metalloproteinases as models of TNF-.alpha. convertase (TACE))  
IT Hydroxamic acids  
RL: BAC (Biological activity or effector, except adverse); BIOL (Biological study)  
(**inhibitors**; comparison of snake venom reprolysin and matrix metalloproteinases as models of TNF-.alpha. convertase (TACE))  
IT Tumor necrosis factor .alpha.  
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)  
(pro-; comparison of snake venom reprolysin and matrix metalloproteinases as models of TNF-.alpha. convertase (TACE))  
IT Enzyme **inhibition** kinetics  
(with hydroxamic acids; comparison of snake venom reprolysin and matrix metalloproteinases as models of TNF-.alpha. convertase (TACE))  
IT 9001-12-1, MMP-8 79955-99-0, MMP-3 146480-35-5, MMP 2 146480-36-6, MMP 9 171715-27-8, Reprolysin  
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BIOL (Biological study); PROC (Process)  
(comparison of snake venom reprolysin and matrix metalloproteinases as models of TNF-.alpha. convertase (TACE))  
IT 140430-53-1 192723-42-5  
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)  
(comparison of snake venom reprolysin and matrix metalloproteinases as models of TNF-.alpha. convertase (TACE))  
IT 151769-16-3, TACE  
RL: BAC (Biological activity or effector, except adverse); BIOL (Biological study)



(models; comparison of snake venom reprotolysin and matrix metalloproteinases as models of TNF-.alpha. convertase (TACE))

- L34 ANSWER 9 OF 12 HCAPLUS COPYRIGHT 2002 ACS  
AN 1996:652046 HCAPLUS  
DN 125:295954  
TI **Substrate** specificity of a novel alcohol resistant metalloproteinase, vimelysin, from *Vibrio* sp. T1800  
AU Takahashi, Saori; Okayama, Kiyooki; Kunugi, Shigeru; Oda, Kohei  
CS Faculty of Textile Science, Kyoto Institute of Technology, Kyoto, 606, Japan  
SO Biosci., Biotechnol., Biochem. (1996), 60(10), 1651-1654  
CODEN: BBBIEJ; ISSN: 0916-8451  
DT Journal  
LA English  
CC 7-3 (Enzymes)  
AB Vimelysin is a novel alc.-resistant metalloproteinase from *Vibrio* sp. T1800. The **substrate** specificity of vimelysin was studied by using natural and furylacryloxy dipeptide **substrates**. Vimelysin cleaved mainly Pro7-Phe8 bonds and slightly Tyr4-Ile5 bonds in human angiotensin I. Vimelysin also cleaved mainly Phe24-Phe25 and Tyr16-Leu17 bonds, and slightly His5-Leu6, His10-Leu11, Ala14-Leu15, and Gly23-Phe24 bonds in oxidized insulin B-chain. The **substrate** specificity of vimelysin, by using furylacryloyl (Fua) dipeptides were also studied. The ratio of kcat/Km for Fua-Gly-Phe-NH2/Fua-Gly-Leu-NH2, Fua-Phe-Leu-NH2/Fua-Gly-Leu-NH2, and Fua-Phe-Phe-NH2/Fua-Gly-Leu-NH2 were 15.9, 27.8, and 59.0, resp. These results indicate that vimelysin easily recognizes phenylalanine in P1' positions, which is different from thermolysin.  
ST **substrate** metalloproteinase vimelysin *Vibrio*; dipeptide cleavage vimelysin *Vibrio*  
IT *Vibrio*  
(**substrate** specificity of a novel alc. resistant metalloproteinase, vimelysin, from *Vibrio* sp. T1800)  
IT 9004-10-8, Insulin, biological studies  
RL: BPR (Biological process); BIOL (Biological study); PROC (Process) (B-chain; alc. resistant metalloproteinase, vimelysin, from *Vibrio* sp. T1800 cleavage of insulin B chain)  
IT 182929-39-1  
RL: BPR (Biological process); BIOL (Biological study); PROC (Process) (alc. resistant metalloproteinase, vimelysin, from *Vibrio* sp. T1800 cleavage of)  
IT 484-42-4  
RL: BPR (Biological process); BIOL (Biological study); PROC (Process) (alc. resistant metalloproteinase, vimelysin, from *Vibrio* sp. T1800 cleavage of angiotensin I)  
IT 26390-02-3 26400-33-9 26400-34-0 110700-76-0  
RL: BPR (Biological process); BIOL (Biological study); PROC (Process) (furylacryloyl dipeptide cleavage by alc. resistant metalloproteinase vimelysin from *Vibrio* sp. T1800)  
IT 176591-17-6, Vimelysin  
RL: PRP (Properties)  
(**substrate** specificity of a novel alc. resistant metalloproteinase, vimelysin, from *Vibrio* sp. T1800)  
  
L34 ANSWER 10 OF 12 HCAPLUS COPYRIGHT 2002 ACS  
AN 1995:466102 HCAPLUS  
DN 122:208637  
TI Reconstructed 19 kDa Catalytic Domain of Gelatinase A Is an Active Proteinase  
AU Ye, Qi-Zhuang; Johnson, Linda L.; Yu, Anita E.; Hupe, Donald  
CS Parke-Davis Pharmaceutical Research Division, Warner-Lambert Company, Ann Arbor, MI, 48105, USA  
SO Biochemistry (1995), 34(14), 4702-8  
CODEN: BICHAW; ISSN: 0006-2960  
DT Journal  
LA English



- CC 7-5 (Enzymes)  
Section cross-reference(s): 13
- AB Matrix metalloproteinases share high protein sequence homol. and have defined domain structures. Gelatinases have a unique 19 kDa fibronectin-like insert in the catalytic domain. A synthetic gene was made to express the catalytic domain of human gelatinase A (GCD), in which two polypeptide fragments of the catalytic domain were joined with deletion of the insert. The synthetic gene was highly expressed in *Escherichia coli*, and the 19 kDa GCD was purified to homogeneity after in vitro refolding. The GCD showed activity at a pH range of 5.5-9 in cleavage of the thiopeptolide Ac-Pro-Leu-Gly-thioester-Leu-Leu-Gly-OEt with optimal activity at neutral pH ( $K_m = 134 \mu\text{M}$  and  $k_{cat} = 16 \text{ s}^{-1}$  at pH 7.0). The activity required both zinc and calcium ions, but high concn. of zinc ion showed **inhibition**. Several stromelysin catalytic domain **inhibitors inhibited** the GCD with similar specificity. The GCD cleaved the fluorogenic peptides Mca-Pro-Leu-Gly-Leu-Dpa-Ala-Arg-NH<sub>2</sub> and Dnp-Pro-Leu-Gly-Leu-Trp-Ala-D-Arg-NH<sub>2</sub> with catalytic efficiency close to full length human gelatinase A. The reconstructed GCD cleaves not only thiopeptolide and peptide **substrates** but also protein **substrates** such as gelatin. These results are consistent with the notion that gelatinases have the same structure for the catalytic domain as other matrix metalloproteinases like stromelysins and **collagenases**.
- ST gelatinase A protein gene synthesis human
- IT Kinetics, enzymic  
Michaelis constant  
Protein sequences  
(reconstructed 19 kDa catalytic domain of gelatinase A is active proteinase)
- IT Gene  
RL: BAC (Biological activity or effector, except adverse); PRP (Properties); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation)  
(reconstructed 19 kDa catalytic domain of gelatinase A is active proteinase)
- IT **Gelatins, biological studies**  
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)  
(reconstructed 19 kDa catalytic domain of gelatinase A is active proteinase)
- IT 7440-66-6, Zinc, biological studies 7440-70-2, Calcium, biological studies 79955-99-0, Stromelysin  
RL: BAC (Biological activity or effector, except adverse); BIOL (Biological study)  
(reconstructed 19 kDa catalytic domain of gelatinase A is active proteinase)
- IT **146480-35-5, Gelatinase A**  
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); RCT (Reactant); BIOL (Biological study); PROC (Process)  
(reconstructed 19 kDa catalytic domain of gelatinase A is active proteinase)
- IT 98992-65-5 121282-17-5 **140430-53-1**  
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)  
(reconstructed 19 kDa catalytic domain of gelatinase A is active proteinase)
- L34 ANSWER 11 OF 12 HCAPLUS COPYRIGHT 2002 ACS
- AN 1992:443338 HCAPLUS
- DN 117:43338
- TI The C-terminal domain of 72 kDa gelatinase A is not required for catalysis, but is essential for membrane activation and modulates interactions with tissue **inhibitors** of metalloproteinases
- AU Murphy, Gillian; Willenbrock, Frances; Ward, Robin V.; Cockett, Mark I.; Eaton, Di; Docherty, Andrew J. P.
- CS Strangeways Res. Lab., Cambridge, CB1 4RN, UK
- SO Biochem. J. (1992), 283(3), 637-41  
CODEN: BIJOAK; ISSN: 0306-3275



DT Journal  
 LA English  
 CC 7-3 (Enzymes)  
 AB Recombinant 72-kDa gelatinase A and a truncated form lacking the C-terminal domain were activated by organomercurials and possessed similar activities toward a no. of **substrates**. The truncated proenzyme differed from the full-length gelatinase in that it could not be activated by a membrane activator and did not bind tissue **inhibitor** of metalloproteinases (TIMP)-2. Kinetic studies also showed that the **inhibition** of the activated truncated enzyme, by both TIMP-1 and TIMP-2, was considerably decreased compared with the full-length enzyme. It was concluded that the C-terminal domain plays an important role in the regulation of gelatinase A by a potential physiol. activator and **inhibitors**.

ST progelatinase A activation domain function; gelatinase A domain interaction TIMP  
 IT Kinetics, enzymic  
 (of gelatinase A and its truncated form, of human)  
 IT Cell membrane  
 (progelatinase A recombinant form of human activation by, enzyme C-terminal domain in)  
 IT **119345-31-2**  
 RL: BIOL (Biological study)  
 (C-terminal domain of recombinant form of, of human, membrane activation in relation to)  
 IT **9040-48-6**, Gelatinase  
 RL: PRP (Properties)  
 (C-terminal domain of, of human, interaction with TIMP-1 and -2 in relation to)  
 IT 124861-55-8, TIMP-2 proteinase **inhibitor** 140208-24-8  
 RL: BIOL (Biological study)  
 (gelatinase A of human **inhibition** by, enzyme C-terminal domain in)  
 IT **140430-53-1**  
 RL: RCT (Reactant)  
 (reaction of, with gelatinase A and truncated form of human, kinetics of)

L34 ANSWER 12 OF 12 HCAPLUS COPYRIGHT 2002 ACS  
 AN 1992:230498 HCAPLUS  
 DN 116:230498  
 TI A novel coumarin-labeled peptide for sensitive continuous assays of the matrix metalloproteinases  
 AU Knight, C. Graham; Willenbrock, Frances; Murphy, Gillian  
 CS Strangeways Res. Lab., Worts Causeway/Cambridge, CB1 4RN, UK  
 SO FEBS Lett. (1992), 296(3), 263-6  
 CODEN: FEBLAL; ISSN: 0014-5793

DT Journal  
 LA English  
 CC 7-1 (Enzymes)  
 AB The peptide deriv. (7-methoxycoumarin-4-yl)Ac-Pro-Leu-Gly-Leu[3-(2,4-dinitrophenyl)-L-2,3-diaminopropionyl]-Ala-Arg-NH<sub>2</sub> (Mca-Pro-Leu-Gly-Leu-Dpa-Ala-Arg-NH<sub>2</sub>) was synthesized as a fluorogenic **substrate** for the matrix metalloproteinases. The highly fluorescent 7-methoxycoumarin group was efficiently quenched by energy transfer to the 2,4-dinitrophenyl group. The punctuated metalloproteinase (PUMP, EC 3.4.24.23) cleaved the **substrate** at the Gly-Leu bond with a 190-fold increase in fluorescence ( $\lambda_{\text{ex}}$  328 nm;  $\lambda_{\text{em}}$  393 nm). In assays of the human matrix metalloproteinases, Mca-Pro-Leu-Gly-Leu-Dpa-Ala-Arg-NH<sub>2</sub> was  $\approx$  50-100-fold more sensitive than dinitrophenyl-Pro-Leu-Gly-Leu-Trp-Ala-D-Arg-NH<sub>2</sub> and continuous assays could be made at enzyme concns. comparable to those used with macromol. **substrates**. Specificity consts. (kcat/Km) were detd. for both synthetic **substrates** with PUMP, **collagenase**, stromelysin, and 72-kDa gelatinase.

ST matrix metalloproteinase continuous detn fluorometry; **collagenase** continuous detn fluorometry; stromelysin continuous detn fluorometry;





gelatinase continuous detn fluorometry; PUMP metalloproteinase continuous  
 detn fluorometry; coumarinyl peptide prepn matrix metalloproteinase detn  
 IT Kinetics, enzymic  
 Michaelis constant  
 (of matrix metalloproteinases, with coumarinyl peptide)  
 IT 70-34-8, 1-Fluoro-2,4-dinitrobenzene  
 RL: ANST (Analytical study)  
 (condensation of, with fluorenylmethoxycarbonylasparagine)  
 IT 71989-16-7  
 RL: ANST (Analytical study)  
 (condensation of, with fluorodinitrobenzene)  
 IT **9001-12-1, Collagenase 9040-48-6, Gelatinase**  
 79955-99-0, Stromelysin 141256-52-2  
 RL: ANT (Analyte); ANST (Analytical study)  
 (detn. and reaction kinetics of, with coumarinyl peptide)  
 IT 140430-54-2P  
 RL: SPN (Synthetic preparation); PREP (Preparation)  
 (prepn. and condensation with (methoxycoumarinyl)acetyl peptide)  
 IT **140430-53-1P**  
 RL: SPN (Synthetic preparation); PREP (Preparation)  
 (prepn. and reaction kinetics with matrix metalloproteinases)  
 IT 140430-55-3P 140430-56-4P  
 RL: SPN (Synthetic preparation); PREP (Preparation)  
 (prepn. of)  
 IT 121282-17-5  
 RL: RCT (Reactant)  
 (reaction of, with matrix metalloproteinases, kinetics of)  
 IT 42382-99-0  
 RL: RCT (Reactant)  
 (reaction of, with methoxycoumarin acetic acid)  
 IT 62935-72-2  
 RL: RCT (Reactant)  
 (reaction of, with prolylleucine Me ester)

=> d his 136-

(FILE 'BIOSIS' ENTERED AT 06:40:25 ON 01 MAR 2002)  
 L36 0 S L11

FILE 'REGISTRY' ENTERED AT 06:40:50 ON 01 MAR 2002

FILE 'HCAPLUS' ENTERED AT 06:41:42 ON 01 MAR 2002  
 L37 2 S L2 AND 9/SC, SX  
 L38 1 S L37 NOT L34  
 L39 5 S L2 AND PROTEIN  
 L40 3 S L39 NOT L34, L38

FILE 'BIOSIS' ENTERED AT 06:43:40 ON 01 MAR 2002  
 E WEITHMAN/AU  
 L41 42 S E8-E10, E12  
 SET COST ON



; Entered [jdelaval 28-Feb-02 16:31]  
09-876091-1  
pjlglarl

; Entered [jdelaval 1-Mar-02 6:32]  
09-876091-2  
pjlglarl

Jan Delaval  
Reference Librarian  
Biotechnology & Chemical Library  
CM1 1E07 - 703-308-4498  
ian.delaval@uspto.gov



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OM protein - protein search, using sw model

Run on: March 1, 2002, 06:51:23 ; Search time 12.65 Seconds  
(without alignments)  
42.152 Million cell updates/sec

Title: 09-876091-2  
Perfect score: 31  
Sequence: 1 plglxar 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 455

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR-68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	54.8	4	2	A32039
2	12	38.7	7	2	S29735
3	12	38.7	7	2	T09512
4	12	38.7	7	2	PT0246
5	12	38.7	7	2	A11483
6	11	35.5	5	2	G44817
7	11	35.5	5	2	I44817
8	11	35.5	5	2	E44817
9	11	35.5	5	2	C44817
10	11	35.5	5	2	A44817
11	11	35.5	7	2	A28340
12	11	35.5	7	2	I48105
13	11	35.5	7	2	I48086
14	11	35.5	7	2	PD0029
15	11	35.5	7	4	S15557
16	10	32.3	4	2	I38888
17	10	32.3	4	2	PT0240
18	10	32.3	4	2	A53284
19	10	32.3	4	2	PT0721
20	10	32.3	5	2	D44823
21	10	32.3	5	2	PT0713
22	10	32.3	6	2	B56979
23	10	32.3	6	2	H48394
24	10	32.3	6	2	A20186
25	10	32.3	6	2	PT0654
26	10	32.3	6	2	PT0621
27	10	32.3	6	2	PT0560
28	10	32.3	6	2	PT0718
29	10	32.3	6	2	PT0589

30	10	32.3	6	2	PT0727	T-cell receptor be
31	10	32.3	6	2	PT0730	T-cell receptor be
32	10	32.3	7	2	S71870	glutathione transf
33	10	32.3	7	2	S42407	glutathione S synth
34	10	32.3	7	2	S09066	globulin IV alpha
35	10	32.3	7	2	S70335	endosperm protein,
36	10	32.3	7	2	A33098	244K exoantigen be
37	10	32.3	7	2	PT0521	T-cell receptor be
38	10	32.3	7	2	PT0529	T-cell receptor be
39	10	32.3	7	2	PT0663	T-cell receptor be
40	10	32.3	7	2	PT0579	T-cell receptor be
41	10	32.3	7	4	PC2056	trichodecenen II -
42	10	32.3	7	4	PC2057	trichodecenen II -
43	9	29.0	4	2	I61883	protamine PI - ora
44	9	29.0	4	2	I37013	protamine PI - Cer
45	9	29.0	4	2	I84439	protamine PI - sav

## ALIGNMENTS

RESULT 1  
A32039  
tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 31-Jul-1989 #sequence\_revision 31-Jul-1989 #text\_change 18-Aug-2000  
C:Accession: A32039  
R:Horvath, A.; Kastlin, A.J.  
J. Biol. Chem. 264, 2175-2179, 1989  
A:Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting fact  
A:Reference number: A32039; MUID:89123285  
A:Accession: A32039  
A:Molecule type: protein  
A:Residues: 1-4 <HOR>  
A:Experimental source: brain  
C:Superfamily: unassigned animal peptides  
C:Keywords: amidated carboxyl end  
F/4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 54.8%; Score 17; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 plg 3  
DB 2 PLG 4  
RESULT 2  
S29735  
polyporphosphate-glucose phosphotransferase (EC 2.7.1.63) - Propionibacterium freudenre  
C:Species: Propionibacterium freudenreichi subsp. shermanii  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 07-May-1999  
C:Accession: S29735  
R:Phillips, N.F.B.; Horn, P.J.; Wood, H.G.  
Arch. Biochem. Biophys. 300, 309-319, 1993  
A:Title: The polyporphosphate- and ATP-dependent glucokinase from Propionibacterium sher  
A:Reference number: S29735; MUID:93143332  
A:Accession: S29735  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <PHI>  
C:Keywords: Phosphotransferase

Query Match 38.7%; Score 12; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.2e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 lgl 4  
DB 4 LGI 6

RESULT 3  
 T09512  
 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - rape mitochondrion (fragment)  
 C:Species: mitochondrion Brassica napus (rape)  
 C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
 C:Accession: T09512  
 R:L'Homme, Y.  
 submitted to the EMBL Data Library, June 1994  
 A:Reference number: Z16706  
 A:Accession: T09512  
 A:Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-7 <LHO>  
 A:Cross-references: EMBL:U10423; NID:g1800190; PID:g1800192  
 C:Genetics: nad5  
 A:Gene: nad5  
 A:Genome: mitochondrion  
 C:Keywords: mitochondrion; NAD; oxidative phosphorylation; oxidoreductase; respiratory

Query Match 38.7%; Score 12; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 2.2e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 1g1 4  
 :||  
 Db 4 1G1 6

RESULT 4  
 PT0246  
 Ig heavy chain CRD3 region (clone 2-103D) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PT0246  
 R:Yamada, M.; Messerman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
 A:Reference number: PT0222; MUID:91108337  
 A:Accession: PT0246  
 A:Molecule type: DNA  
 A:Residues: 1-7 <YAM>  
 A:Experimental source: B lymphocyte  
 C:Keywords: heterotrimer; immunoglobulin

Query Match 38.7%; Score 12; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 2.2e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 1g1 4  
 :||  
 Db 4 1G1 6

RESULT 5  
 A11483  
 aspartate transaminase (EC 2.6.1.1), mitochondrial - sheep (fragment)  
 N:Alternate names: aspartate aminotransferase, mitochondrial  
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C:Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 20-Aug-1999  
 C:Accession: A11483  
 R:Campos-Cavieles, M.; Milstein, C.P.  
 Biochem. J. 147, 275-281, 1975  
 A:Title: The sequences of the coenzyme-binding peptide in the cytoplasmic and the mitoch  
 A:Reference number: A11483; MUID:76039441  
 A:Accession: A11483  
 A:Molecule type: protein  
 A:Residues: 1-7 <CAM>  
 A:Experimental source: liver  
 C:Keywords: aminotransferase; mitochondrion; phosphoprotein; pyridoxal phosphate

F:2/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 38.7%; Score 12; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 2.2e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 1g1 4  
 :||  
 Db 4 MGL 6

RESULT 6  
 G44817  
 27.5 kDa structural protein - Leuconostoc oenos phage P32 (fragment)  
 C:Species: Leuconostoc oenos phage P32  
 C:Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C:Accession: G44817  
 R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
 J. Gen. Microbiol. 137, 2135-2139, 1991  
 A:Title: Lysogeny in Leuconostoc oenos.  
 A:Reference number: A44817; MUID:92085033  
 A:Accession: G44817  
 A:Molecule type: protein  
 A:Residues: 1-5 <ARE>  
 A>Note: sequence extracted from NCBI backbone (NCBIP:70333)

Query Match 35.5%; Score 11; DB 2; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.2e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 1g1 4  
 :||  
 Db 3 VGL 5

RESULT 7  
 I44817  
 27.5K structural protein - Leuconostoc oenos phage P37 (fragment)  
 C:Species: Leuconostoc oenos phage P37  
 C:Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C:Accession: I44817  
 R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
 J. Gen. Microbiol. 137, 2135-2139, 1991  
 A:Title: Lysogeny in Leuconostoc oenos.  
 A:Reference number: A44817; MUID:92085033  
 A:Accession: I44817  
 A:Molecule type: protein  
 A:Residues: 1-5 <ARE>  
 A>Note: sequence extracted from NCBI backbone (NCBIP:70330)

Query Match 35.5%; Score 11; DB 2; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.2e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 1g1 4  
 :||  
 Db 3 VGL 5

RESULT 8  
 E44817  
 27.5K structural protein - Leuconostoc oenos phage P54 (fragment)  
 C:Species: Leuconostoc oenos phage P54  
 C:Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
 C:Accession: E44817  
 R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
 J. Gen. Microbiol. 137, 2135-2139, 1991  
 A:Title: Lysogeny in Leuconostoc oenos.  
 A:Reference number: A44817; MUID:92085033  
 A:Accession: E44817

A:Molecule type: protein  
A:Residues: 1-5 <ARE>  
A:Note: sequence extracted from NCBI backbone (NCBIP:70336)

Query Match 35.5%; Score 11; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.2e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 1g1 4  
: 1  
: 1  
Db 3 VGL 5

RESULT 9  
C44817  
28.5K structural protein - Leuconostoc oenos phage P4C5-12 (fragment)  
C:Species: Leuconostoc oenos phage P4C5-12  
C:Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
C:Accession: C44817  
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
J. Gen. Microbiol. 137, 2135-2139, 1991  
A:Title: Lysogeny in Leuconostoc oenos.  
A:Reference number: A44817; MUID:92085033  
A:Accession: C44817  
A:Molecule type: protein  
A:Residues: 1-5 <ARE>  
A:Note: sequence extracted from NCBI backbone (NCBIP:70341)

Query Match 35.5%; Score 11; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.2e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 1g1 4  
: 1  
: 1  
Db 3 VGL 5

RESULT 10  
A44817  
28K structural protein - Leuconostoc oenos phage P4C11-15 (fragment)  
C:Species: Leuconostoc oenos phage P4C11-15  
C:Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
C:Accession: A44817  
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
J. Gen. Microbiol. 137, 2135-2139, 1991  
A:Title: Lysogeny in Leuconostoc oenos.  
A:Reference number: A44817; MUID:92085033  
A:Accession: A44817  
A:Molecule type: protein  
A:Residues: 1-5 <ARE>  
A:Note: sequence extracted from NCBI backbone (NCBIP:70343)

Query Match 35.5%; Score 11; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.2e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 1g1 4  
: 1  
: 1  
Db 3 VGL 5

RESULT 11  
A28340  
myomodulin - California sea hare  
C:Species: Aplysia californica (California sea hare)  
C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 18-Jun-1993  
C:Accession: A28340  
R:Cropper, E.C.; Tenenbaum, R.; Kolks, M.A.G.; Kupfermann, I.; Weiss, K.R.  
Proc. Natl. Acad. Sci. U.S.A. 84, 5483-5486, 1987  
A:Title: Myomodulin: A bioactive neuropeptide present in an identified cholinergic buccal

A:Reference number: A28340; MUID:87261010  
A:Accession: A28340  
A:Molecule type: protein  
A:Residues: 1-7 <CRO>

Query Match 35.5%; Score 11; DB 2; Length 7;  
Best Local Similarity 25.0%; Pred. No. 2.2e+05;  
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 1g1 4  
: 1  
: 1  
Db 1 PWSM 4

RESULT 12  
I48105  
dihydrofolate reductase - Chinese hamster (fragment)  
C:Species: Cricetus griseus (Chinese hamster)  
C:Date: 04-Sep-1997 #sequence\_revision 07-Nov-1997 #text\_change 05-Nov-1999  
C:Accession: I48105  
R:Azizkhan, J.C.; Vaughn, J.P.; Christy, R.J.; Hamlin, J.L.  
Biochemistry 25, 6228-6236, 1986  
A:Title: Nucleotide sequence and nuclease hypersensitivity of the Chinese hamster dh  
A:Reference number: I48105; MUID:87076541  
A:Accession: I48105  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-7 <RES>  
A:Cross-references: GB:M14771; NID:g191055; PIDN:AAA36975.1; PID:g191056

Query Match 35.5%; Score 11; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 1g1 2  
: 1  
: 1  
Db 4 PL 5

RESULT 13  
I48086  
DNA topoisomerase II alpha - Chinese hamster (fragment)  
C:Species: Cricetus griseus (Chinese hamster)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: I48086  
R:Ng, S.W.; Eder, J.P.; Schnipper, L.E.; Chan, V.T.W.  
J. Biol. Chem. 270, 25850-25858, 1995  
A:Title: Molecular cloning and characterization of the promoter for the Chinese hamst  
A:Reference number: I48086; MUID:96029684  
A:Accession: I48086  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-7 <RES>  
A:Cross-references: EMBL:U34196; NID:g1041231; PIDN:AMC52315.1; PID:g1041232

Query Match 35.5%; Score 11; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.2e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 1g1 2  
: 1  
: 1  
Db 5 PL 6

RESULT 14  
PD0029  
pev-kinin 1 - penaeid shrimp (Penaeus vannamei) (fragment)  
C:Species: Penaeus vannamei  
C:Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 19-May-2000  
C:Accession: PD0029

R:Nieto, J.; Vaeleart, D.; Derna, R.; Waelkens, E.; Cersliens, A.; Coast, G.; Devreese, Biochem. Biophys. Res. Commun. 248, 406-411, 1998  
A:Title: Identification of one tachykinin- and two kinin-related peptides in the brain  
A:Reference number: PD0027; MUID:96342103  
A:Accession: PD0029  
A:Molecule type: protein  
A:Residues: 1-7 <NIE>  
C:Comment: This peptide belongs to myotropic neuropeptides.

Query Match 35.5%; Score 11; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.2e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 plg 3  
| |  
DB 5 PRG 7

## RESULT 15

orf4 rara 5'-region - human  
S15597  
C:Species: Homo sapiens (man)  
C:Date: 04-Jun-1999 #sequence\_revision 04-Jun-1999 #text\_change 28-Jun-1999  
C:Accession: S15597  
R:Brand, N.J.; Petkovich, M.; Chamoun, P.  
Nucleic Acids Res. 18, 6799-6806, 1990  
A:Title: Characterization of a functional promoter for the human retinoic acid receptor  
A:Reference number: S15594; MUID:91088249  
A:Accession: S15597  
A:Molecule type: DNA  
A:Residues: 1-7 <BR>  
A:Cross-references: EMBL:X56058; NID:935876  
A:Note: this ORF from Fig. 2 is not annotated in GenBank entry HSRARA2, release 111.0  
C:Comment: This sequence is not thought to be translated.  
C:Genetics:  
A:Gene: GDB:RARA  
A:Cross-references: GDB:120337; OMIM:180240  
A:Map position: 17q12-17q12

Query Match 35.5%; Score 11; DB 4; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.2e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 plg 3  
| |  
DB 2 PRG 4

Search completed: March 1, 2002, 06:53:15  
Job time: 112 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2002, 06:52:58 ; Search time 10.16 Seconds  
(without alignments)  
25.261 Million cell updates/sec

Title: 09-876091-2  
Perfect score: 31  
Sequence: 1 p1g1xar 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues  
Total number of hits satisfying chosen parameters: 74

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	35.5	6	VP19_HSV1K	P23210 herpes simp
2	11	35.5	7	MNP1_LEPDE	P42984 leptinotars
3	11	35.5	7	MYOM_APLCA	P15513 aplysia cal
4	10	32.3	5	AL14_CARMA	P81817 carcinus ma
5	10	32.3	6	TMOE_SARBU	P41495 sarcophaga
6	10	32.3	7	AL12_CARMA	P81805 carcinus ma
7	10	32.3	7	AL13_CARMA	P81806 carcinus ma
8	10	32.3	7	AL14_CARMA	P81807 carcinus ma
9	10	32.3	7	AL15_CARMA	P81808 carcinus ma
10	10	32.3	7	AL17_CYPDO	P82158 cydia pomon
11	9	29.0	5	BIOB_SALTY	P12678 salmonella
12	9	29.0	6	CIP1_MYTED	P13737 mytilus edu
13	9	29.0	6	CIP2_MYTED	P13737 mytilus edu
14	9	29.0	7	CARP_MYTED	P10420 mytilus edu
15	9	29.0	7	UHL1_RAT	P56576 rattus norv
16	8	25.8	4	DCML_PSECH	P19916 pseudomonas
17	8	25.8	5	UF01_MOUSE	P38639 mus muscula
18	7	22.6	3	THYL_PIG	P01151 sus scrofa
19	7	22.6	4	EOS1_HUMAN	P02731 homo sapien
20	7	22.6	4	RM01_YEAST	P36515 saccharomyc
21	7	22.6	4	TUFT_HUMAN	P01858 homo sapien
22	7	22.6	5	BPP7_BOTIN	P30425 bothrops in
23	7	22.6	5	PAP2_PARMA	P81864 pardachirus
24	7	22.6	5	PRCT_PERAM	P01373 periplaneta
25	7	22.6	5	SUGA_ACHDO	P19991 acheta dome
26	7	22.6	5	TP15_CANFA	P34774 canis famli
27	7	22.6	6	OVN_LEPDE	P42985 leptinotars
28	7	22.6	6	TRP1_PSEPU	P36414 pseudomonas
29	7	22.6	7	CHOX_ALCSP	P16101 alcaligenes
30	7	22.6	7	FAR1_HELTI	P41871 helisoma tr
31	7	22.6	7	FAR4_PANRE	P41875 panagrellus
32	7	22.6	7	FAR5_HIRME	P42354 hirudo medi
33	7	22.6	7	FARB_CALVO	P41866 calliphora

## ALIGNMENTS

34	7	22.6	7	1	GFRP_MOUSE	P99025 mus musculu
35	7	22.6	7	1	LANC_CAROI	P36960 carnobacter
36	7	22.6	7	1	UF04_MOUSE	P38642 mus musculu
37	7	22.6	7	1	UN06_PINPS	P81675 pinus pinas
38	6	19.4	3	1	GRMM_HUMAN	P01157 homo sapien
39	6	19.4	4	1	ACH1_ACHFU	P35904 achatina fu
40	6	19.4	4	1	DCMS_PSECH	P19918 pseudomonas
41	6	19.4	5	1	UXA4_CHLTR	P38005 chlamydia t
42	6	19.4	6	1	FARP_MONEX	P41966 moniezia ex
43	6	19.4	6	1	LOK1_LOCOM	P41491 locusta mig
44	6	19.4	7	1	IGAO_DACDE	P06294 dactylium d
45	6	19.4	7	1	UC24_MAIZE	P00630 zea mays (m

RESULT 1	VP19_HSV1K	STANDARD;	PRT;	6 AA.
ID	VP19_HSV1K			
AC	P23210;			
DT	01-NOV-1991 (Rel. 20, Created)			
DT	01-NOV-1991 (Rel. 20, Last sequence update)			
DT	01-DEC-1992 (Rel. 24, Last annotation update)			
DE	CAPSID ASSEMBLY AND DNA MATURATION PROTEIN (VIRION PROTEIN UL38)			
DE	(CAPSID PROTEIN VP19C) (FRAGMENT).			
GN	UL38.			
OS	Herpes simplex virus (type 1 / strain KOS).			
OC	viruses; dsDNA viruses; no RNA stage; Herpesviridae;			
OC	Alphaherpesvirinae; Simplexvirus.			
OX	NCBI_TaxID=10306;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91101287; PubMed=1846198;			
RA	Flanagan M.M., Papavasiliou A.G., Rice M., Hecht L.B.,			
RA	Silverstein S., Wagner E.K.;			
RT	"Analysis of the herpes simplex virus type 1 promoter controlling the			
RT	expression of UL38, a true late gene involved in capsid assembly.";			
RL	J. Virol. 65:769-786(1991).			
CC	-1- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE			
CC	EMBEDDED. BINDS DNA.			
CC	-1- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL: M57646; AAA5830.1; -			
KW	Capsid assembly; Coat protein; DNA-binding.			
FT	NON_TER 6 6			
SQ	SEQUENCE 6 AA: 703 MW: 67376451A336F000 CRC64;			

Query Match	35.5%	Score 11;	DB 1;	Length 6;
Best Local Similarity	100.0%	Pred. No. 1e+05;		
Matches 2;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	1 p1 2
Db	5 pL 6

RESULT 2	MNP1_LEPDE	STANDARD;	PRT;	7 AA.
ID	MNP1_LEPDE			
AC	P42984;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	01-NOV-1995 (Rel. 32, Last annotation update)			

```

DE MYOTROPIC NEUROPEPTIDE 1 (LED-MNP-1).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Phyltophaga; Chrysomeloidea; Chrysomelidae;
OC Chrysomelinae; Leptinotarsa.
OX NCBI_TaxID=75339;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-Head;
RX MEDLINE=95380343; PubMed=7651886;
RA Splitaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
RA Grauwels L., van Leuven F., de Loof A.;
RT "Identification, characterization, and immunological localization of
RT a novel myotropic neuropeptide in the Colorado potato beetle,
RT Leptinotarsa decemlineata."
RL Peptides 16:365-374(1995).
CC -1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
CC CC
CC Neuropeptide; Amidation.
CC KW MOD.RES 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;
SQ SEQUENCE 7 AA; 847 MW; 6734072685B68700 CRC64;

Query Match 35.5%; Score 11; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 pl 2
DB 5 PL 6

RESULT 3
MYOM_APLCA STANDARD: PRT; 7 AA.
ID MYOM_APLCA
AC P15513;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE MYOMODULIN (NEURON B16 PEPTIDE).
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspeida;
OC Aplysiidae; Aplysia.
OX NCBI_TaxID=65500;
RN [1]
RP SEQUENCE.
RC TISSUE=Buccal muscle;
RX MEDLINE=87261010; PubMed=3474664;
RA Cropper E.C., Tenenbaum R., Kolks M.A.G., Kuffermann I., Weiss K.R.;
RT "Myomodulin: a bioactive neuropeptide present in an identified
RT cholinergic buccal motor neuron of Aplysia."
RL Proc. Natl. Acad. Sci. U.S.A. 84:5483-5486(1987).
CC -1- FUNCTION: EXOGENOUS APPLICATION OF THE PEPTIDE POTENTIATES ARC
CC MUSCLE CONTRACTIONS.
CC DR PIR: A28340; A28340.
CC KW Neuropeptide; Amidation.
FT MOD.RES 7 AA; 847 MW; 6734072685B68700 CRC64;
SQ SEQUENCE 7 AA; 847 MW; 6734072685B68700 CRC64;

Query Match 35.5%; Score 11; DB 1; Length 7;
Best Local Similarity 25.0%; Pred. No. 1e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 pl 1 4
DB 1 PMSM 4

RESULT 4
AL14_CARMA STANDARD: PRT; 5 AA.
ID AL14_CARMA

```

```

AC P81817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINOSTATIN 14.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Dye H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
CC CC
CC Neuropeptide; Amidation; Multigene family.
CC KW MOD.RES 5 AA; 586 MW; 672879D5AB300000 CRC64;
SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 32.3%; Score 10; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 pl 4
DB 4 GL 5

RESULT 5
TMOF_SARBU STANDARD: PRT; 6 AA.
ID TMOF_SARBU
AC P41495;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE TRYPSIN-MODULATING OOSTATIC FACTOR (TMOF).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidea; Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-Ovary;
RX MEDLINE=94211930; PubMed=8159807;
RA Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
RA de Loof A.;
RT "Sequencing and characterization of trypsin modulating oostatic
RT factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria
RT (Sarcophaga) bullata."
RL Regul. Pept. 50:61-72(1994).
CC -1- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
CC IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
CC CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCYTE
CC DEVELOPMENT.
CC CC
CC -1- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
CC EPITHELIUM AFTER A BLOOD MEAL.
CC KW Hormone.
FT MOD.RES 6 AA; 695 MW; 61E72451B7642000 CRC64;
SQ SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;

Query Match 32.3%; Score 10; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 pl 1 4

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Db 2 PTNL 5

```
RESULT 6
ALL2_CARMA STANDARD; PRT: 7 AA.
ID ALL2_CARMA
AC P81805;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE CARCINUSSTATIN 2.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KM Neuropeptide; Amidation; Multigene family.
FT MOD_RES 7
SO SEQUENCE 7 AA; 770 MW; 672879CDBC85DBD70 CRC64;
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Query Match 32.3%; Score 10; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 91 4  
||  
Db 6 GL 7

```
RESULT 7
ALL3_CARMA STANDARD; PRT: 7 AA.
ID ALL3_CARMA
AC P81806;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE CARCINUSSTATIN 3.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KM Neuropeptide; Multigene family.
FT MOD_RES 7
SO SEQUENCE 7 AA; 796 MW; 672879CDBC8476B70 CRC64;
```

Query Match 32.3%; Score 10; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 91 4  
||  
Db 6 GL 7

```
RESULT 8
ALL4_CARMA STANDARD; PRT: 7 AA.
ID ALL4_CARMA
AC P81807;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE CARCINUSSTATIN 4.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KM Neuropeptide; Multigene family.
FT MOD_RES 7
SO SEQUENCE 7 AA; 782 MW; 672879CDBC8476AC0 CRC64;
```

Query Match 32.3%; Score 10; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 91 4  
||  
Db 6 GL 7

```
RESULT 9
ALL5_CARMA STANDARD; PRT: 7 AA.
ID ALL5_CARMA
AC P81808;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE CARCINUSSTATIN 5.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KM Neuropeptide; Amidation; Multigene family.
FT MOD_RES 7
SO SEQUENCE 7 AA; 781 MW; 672879CDBC8476420 CRC64;
```

Query Match 32.3%; Score 10; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 gl 4  
11  
DB 6 GL 7

RESULT 10

ALL7\_CYPDPO STANDARD; PRT; 7 AA.  
ID ALL7\_CYPDPO  
AC P82158;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE CYDIASTATIN 7.  
OS Cydia pomonella (Coddling moth).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.  
OX NCBI\_TaxID=82600;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Larva;  
RX MEDLINE=98054539; PubMed=9392829;  
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
RT "Lepidopteran peptides of the allatostatin superfamily."  
RL Peptides 18:1301-1309(1997).  
CC -I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 7  
SQ SEQUENCE 7 AA; 873 MW; 672879CABB569350 CRC64;

Query Match 32.3%; Score 10; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 gl 4  
11  
DB 6 GL 7

RESULT 11

BIOB\_SALTY STANDARD; PRT; 5 AA.  
ID BIOB\_SALTY  
AC P12678;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE) (FRAGMENT).  
GN BIOB.  
OS Salmonella typhimurium.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Salmonella.  
OX NCBI\_TaxID=602;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89006280; PubMed=2971595;  
RA Shivan D., Campbell A.;  
RT "Transcriptional regulation and gene arrangement of Escherichia coli,  
RT Citrobacter freundii and Salmonella typhimurium biotin operons."  
RL Gene 67:203-211(1988).  
CC -I- CATALYTIC ACTIVITY: DEHYDROBIOTIN + (S) = BIOTIN.  
CC -I- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.  
CC -I- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES  
FAMILY.

-----  
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-----

DR EMBL: M21923; -, NOT\_ANNOTATED\_CDS.  
DR StyGene; SG10027; bioB.  
KW Biotin biosynthesis; Iron-sulfur; Transferase.  
FT NON\_TER 5  
SQ SEQUENCE 5 AA; 611 MW; 7761F40DD6F00000 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ar 7  
11  
DB 2 AR 3

RESULT 12

CIP1\_MYTED STANDARD; PRT; 6 AA.  
ID CIP1\_MYTED  
AC P13736;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE CONTRACTION-INHIBITING PEPTIDE I (MIP I).  
OS Mytilus edulis (Blue mussel).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
OC Mytiloidea; Mytilidae; Mytilus.  
OX NCBI\_TaxID=6550;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=pedal ganglion;  
RX MEDLINE=88240357; PubMed=3377776;  
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Munesoka Y.;  
RT "Structures and actions of Mytilus inhibitory peptides."  
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).  
CC -I- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN  
MUSCLES.  
CC -I- SIMILARITY: TO MIP II.  
DR PIR: A27696; A27696.  
KW Hormone; Amidation.  
FT MOD\_RES 6  
SQ SEQUENCE 6 AA; 637 MW; 72C9C68775B81000 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 6;  
Best Local Similarity 50.0%; Pred. No. 1e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 pl 2  
1:  
DB 3 PM 4

RESULT 13

CIP2\_MYTED STANDARD; PRT; 6 AA.  
ID CIP2\_MYTED  
AC P13737;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE CONTRACTION-INHIBITING PEPTIDE II (MIP II).  
OS Mytilus edulis (Blue mussel).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
OC Mytiloidea; Mytilidae; Mytilus.  
OX NCBI\_TaxID=6550;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=pedal ganglion;  
RX MEDLINE=88240357; PubMed=3377776;

RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.,  
 RT "Structures and actions of Mytilus inhibitory peptides."  
 RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).  
 CC -I- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN  
 CC MUSCLES.  
 CC -I- SIMILARITY: TO MIP I.  
 DR PIR: B27696; B27696.  
 KW Hormone; Amidation.  
 FT MOD\_RES 6  
 SQ SEQUENCE 6 AA; 621 MW; 72C9C6876DD81000 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 pl 2  
 1;  
 Db 3 PM 4

RESULT 14  
 CARP\_MYTED  
 ID CARP\_MYTED STANDARD; PRT; 7 AA.  
 AC P10420;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 01-MAR-1989 (Rel. 10, Last annotation update)  
 DE CATCH-RELAXING PEPTIDE (CARP).  
 OS Mytilus edulis (Blue mussel).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
 OC Mytiloidea; Mytilidae; Mytilus.  
 OX NCBI\_TaxID=6550;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=86052022; PubMed=3676797;  
 RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,  
 RA Muneoka Y.;  
 RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia."  
 RL Brain Res. 422:374-376(1987).  
 CC -I- FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)  
 CC AND INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS  
 CC RETRACTOR MUSCLE.  
 CC PIR: A29342; ECMUCR.  
 KW Hormone; Amidation.  
 FT MOD\_RES 7  
 SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 pl 2  
 1;  
 Db 3 PM 4

RESULT 15  
 UH11\_RAT  
 ID UH11\_RAT STANDARD; PRT; 7 AA.  
 AC P56576;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF HEART TISSUE (SPOT P11) (FRAGMENT).  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=WISTAR; TISSUE=Heart;

RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,  
 RA Jungblut P.R.;  
 RL Submitted (SEP-1998) to the SWISS-PROT data bank.  
 CC -I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 8.5, ITS MW IS: 42 KDA.  
 CC UNSURE 2 2 OR A.  
 FT NON\_TER 7 7  
 FT SEQUENCE 7 AA; 775 MW; 6866DB040DC5A6B0 CRC64;

Query Match 29.0%; Score 9; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 ar 7  
 1;  
 Db 3 AR 4

Search completed: March 1, 2002, 06:55:57  
 Job time: 179 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2002, 06:52:38 ; Search time 21.97 Seconds  
(without alignments)  
46.605 Million cell updates/sec

Title: 09-876091-2  
Perfect score: 31  
Sequence: 1 p1g1xar 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 65

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPREMBL\_17:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mmc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	35.5	7	10	P93233 lycopersico
2	11	35.5	7	10	P93233 lycopersico
3	10	32.3	7	10	O9C5B3 arabidopsi
4	10	32.3	7	11	O63668 ratius norv
5	9	29.0	5	13	P82099 litoria rub
6	9	29.0	6	13	P82096 litoria rub
7	8	25.8	7	2	O50556 actinobacil
8	7	22.6	5	13	P82073 litoria rub
9	7	22.6	7	2	O47029 enterobacte
10	7	22.6	7	4	O15897 homo sapien
11	7	22.6	7	8	P92421 psathyrosta
12	7	22.6	7	8	P92385 hordeum mar
13	7	22.6	7	8	P92210 agropyron c
14	7	22.6	7	8	P92214 amblyopyrum
15	7	22.6	7	8	P92218 australopyr
16	7	22.6	7	8	P92221 bromus ther
17	7	22.6	7	8	P92226 crilnopsi
18	7	22.6	7	8	P92372 haynaldia v
19	7	22.6	7	8	P92381 hordeum bra

ID	Score	Query Match	Length	ID	Description
20	7	22.6	7	8	P92387 henrardia p
21	7	22.6	7	8	P92390 heteranthel
22	7	22.6	7	8	P92393 hordeum vul
23	7	22.6	7	8	P92425 pseudoroegn
24	7	22.6	7	8	P92427 peridictyon
25	7	22.6	7	8	P92430 aegilops ta
26	7	22.6	7	8	P92442 taeniattheru
27	7	22.6	7	8	P92440 thnopyrum
28	7	22.6	7	8	P92403 lophopyrum
29	7	22.6	7	8	O98866 spiniacia ol
30	7	22.6	7	10	P82445 nicotiana t
31	7	22.6	7	12	O66113 cherry leat
32	7	22.6	7	12	O07624 rous sarcom
33	7	22.6	7	13	P82065 litoria rub
34	7	22.6	7	13	P82101 litoria rub
35	6	19.4	6	10	P82181 spiniacia ol
36	6	19.4	6	10	P82182 spiniacia ol
37	6	19.4	7	2	O47505 escherichia
38	6	19.4	7	2	O47477 escherichia
39	6	19.4	7	4	O15903 homo sapien
40	6	19.4	7	10	O49223 glycine max
41	6	19.4	7	11	O63480 ratius norv
42	6	19.4	7	11	O55184 ratius norv
43	5	16.1	6	10	P82541 spiniacia ol
44	5	16.1	7	2	O07354 synechococc
45	5	16.1	7	12	O9y199 human adeno

## ALIGNMENTS

RESULT 1  
P93233 PRELIMINARY: PRT: 7 AA.  
AC P93233:  
DT 01-MAY-1997 (TREMBLrel. 03, Created)  
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE (EC 4.4.1.14) (ACC.  
DE SYNTHASE) (FRAGMENT).  
GN LE-ACSB.  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4081;  
RN [1]  
RP  
RX MEDLINE=97351561; PubMed=9207843;  
RA Oetiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;  
RT "Differential induction of seven 1-aminocyclopropane-1-carboxylate  
RT synthase genes by elicitor in suspension cultures of tomato  
RT (Lycopersicon esculentum).";  
RL Plant Mol. Biol. 34:275-286(1997).  
CC -I- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE = 1-  
CC AMINOCYCLOPROPANE-1-CARBOXYLATE + METHYLTHIOADENOSINE.  
DR EMBL: U75692; AAC49682.1; -;  
KW Lyase.  
FT NON\_TER 1 1  
SQ SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;

Query Match 35.5%; Score 11; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.7e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 p1 2  
11  
Db 3 PL 4

RESULT 2

042564  
ID 042564 PRELIMINARY: PRT: 7 AA.  
AC 042564:  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE TRUNCATED VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT (FRAGMENT).  
GN SCN8A.  
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Takifugu.  
OX NCBI\_TaxID=31033;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-97442476; PubMed-9295353;  
RA Plummer N.W., McBurney M.W., Weisler M.H.;  
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated  
RT two-domain protein in fetal brain and non-neuronal cells.";  
RL J. Biol. Chem. 272:24008-24015(1997).  
DR EMBL: U97673; AAB80916.1; -.  
KM Ionic channel.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 35.5%; Score 11; DB 13; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.7e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 p1 2  
11  
DB 2 p1 3

RESULT 3  
ID 09C5B3 PRELIMINARY: PRT: 7 AA.  
AC 09C5B3:  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE HYPOTHETICAL 0.7 KDA PROTEIN (FRAGMENT).  
GN DIDI 10A-2B.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=ROOTS;  
RX MEDLINE-21171025; PubMed-11277426;  
RA Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;  
RT "Arabidopsis thaliana genes expressed in the early compatible  
RT interaction with root-knot nematodes.";  
RL Mol. Plant Microbe Interact. 14:288-299(2001).  
DR EMBL: AJ286350; CAB71014.2; -.  
KM Hypothetical protein.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 719 MW; 6732C7287EB325D0 CRC64;

Query Match 32.3%; Score 10; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.7e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 p1 4  
11  
DB 4 GL 5

RESULT 4  
ID 063668 PRELIMINARY: PRT: 7 AA.  
AC 063668:  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE VASOPRESSIN V2 RECEPTOR.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY;  
RX MEDLINE-95396550; PubMed-7667072;  
RA Mandon B., Bellanger A.C., Elalouf J.M.;  
RT "Inverse PCR-mediated cloning of the promoter for the rat vasopressin  
RT V2 receptor gene.";  
RL Pfluegers Arch. 430:12-18(1995).  
DR EMBL: X83264; CAA58237.1; -.  
SQ SEQUENCE 7 AA; 703 MW; 75A767287DC6D6F0 CRC64;

Query Match 32.3%; Score 9; DB 13; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.7e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 p1 4  
11  
DB 4 GL 5

RESULT 5  
ID P82099 PRELIMINARY: PRT: 5 AA.  
AC P82099:  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
DE ELECTRIN 3.  
OS Litorea rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=SKIN SECRETION;  
RX Wabnitz P.A., Bowle J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
RT Litorea rubella. Comparison with the skin peptides from Litorea  
RT rubella.";  
RL Aust. J. Chem. 52:0-0(1999).  
KW Amphibian skin; Amidation.  
FT MOD\_RES  
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 29.0%; Score 9; DB 13; Length 5;  
Best Local Similarity 50.0%; Pred. No. 4.7e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 p1 2  
11  
DB 4 PM 5

RESULT 6  
ID P82096 PRELIMINARY: PRT: 6 AA.  
AC P82096:



DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE ELECTRIN 1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
OC Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=SKIN SECRETION;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
RT Litoria electrica. Comparison with the skin peptides from Litoria  
RT rubella.";  
RL Aust. J. Chem. 52:0-0(1999).  
KW Amphibian skin; Amidation.  
FT MOD\_RES 6 AA; 792 MW; 6683704772C9A000 CRC64;  
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 29.0%; Score 9; DB 13; Length 6;  
Best Local Similarity 50.0%; Pred. No. 4.7e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 pl 2  
1;  
Db 3 pl 4

RESULT 7  
ID 050556 PRELIMINARY; PRT; 7 AA.  
AC 050556;  
DT 01-JUN-1998 (TREMBlrel. 06, Created)  
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE GLYA (FRAGMENT).  
GN GLYA.  
OS Actinobacillus actinomycetemcomitans (Haemophilus  
OS actinomycetemcomitans).  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OC Actinobacillus.  
OX NCBI\_TaxID=714;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 33384;  
RX MEDLINE=96355846; PubMed=8751884;  
RA Kolodrubetz D., Spltznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,  
RA Kraig E.;  
RT "cis Elements and trans factors are both important in strain-specific  
RT regulation of the leukotoxin gene in Actinobacillus  
RT actinomycetemcomitans.";  
RL Infect. Immun. 64:3451-3460(1996).  
DR EMBL; U51862; AAB88721.1; -;  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 25.8%; Score 8; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 4.7e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 pl 2  
1;  
Db 4 pl 5

RESULT 8  
ID P82073 PRELIMINARY; PRT; 5 AA.  
AC P82073;

DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE RUBELLIDIN 3.2.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
OC Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=SKIN SECRETION;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
RT Litoria electrica. Comparison with the skin peptides from Litoria  
RT rubella.";  
RL Aust. J. Chem. 52:0-0(1999).  
CC -I- FUNCTION: CARIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR  
CC ANTIBIOTIC ACTIVITY.  
CC -I- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.  
KW Amphibian skin.  
FT SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;  
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 22.6%; Score 7; DB 13; Length 5;  
Best Local Similarity 50.0%; Pred. No. 4.7e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 lg 3  
1  
Db 1 VG 2

RESULT 9  
ID 047029 PRELIMINARY; PRT; 7 AA.  
AC 047029;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)  
DE AAD A1 PROTEIN (FRAGMENT).  
GN AAD A1.  
OS Enterobacter cloacae.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Enterobacter.  
OX NCBI\_TaxID=550;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=94079349; PubMed=8257126;  
RX Rather P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.J.;  
RA "Analysis of the aac(3)-Via gene encoding a novel 3-N-  
RT acetyltransferase.";  
RL Antimicrob. Agents Chemother. 37:2074-2079(1993).  
DR EMBL; M88012; AAA16193.1; -;  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 744 MW; 633862DC321A030 CRC64;

Query Match 22.6%; Score 7; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 4.7e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 lg 3  
1  
Db 5 VG 6

RESULT 10  
ID 015897 PRELIMINARY; PRT; 7 AA.  
AC 015897;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)  
 DE (CLONE XP6A11A) (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RA Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
 RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,  
 RA Caskey C.T.H.,  
 RL Hum. Mol. Genet. 0:0-0(0).  
 DR EMBL: L32077; AAA73887.1; -.  
 FT NON\_TER 1 1  
 FT SEQUENCE 7 AA; 814 MW; 67281DD3372046B0 CRC64;  
 SQ

Query Match 22.6%; Score 7; DB 4; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 4.7e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 1x a 6  
 DB 3 LKA 5

RESULT 11  
 P92421  
 ID P92421 PRELIMINARY; PRT; 7 AA.  
 AC P92421;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last annotation update)  
 DE RIBOSOMAL PROTEIN 11 (FRAGMENT).  
 GN RPS11.  
 OS Psathyrostachys fragilis.  
 OC Chloroplast.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 CC Triticeae; Psathyrostachys.  
 OX NCBI\_TaxId=37729;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H4372, AND H917; TISSUE=LEAVES;  
 RA Petersen G., Seberg O.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Z77753; CAB01337.1; -.  
 DR EMBL: Z77752; CAB01334.1; -.  
 KW Ribosomal protein; Chloroplast.  
 FT NON\_TER 1 1  
 FT SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;  
 SQ

Query Match 22.6%; Score 7; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 P 1  
 DB 1 P 1

RESULT 12  
 P92385  
 ID P92385 PRELIMINARY; PRT; 7 AA.  
 AC P92385;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last annotation update)  
 DE RIBOSOMAL PROTEIN 11 (FRAGMENT).  
 GN RPS11.

OS Hordeum maritimum (Seaside barley).  
 OC Chloroplast.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 CC Triticeae; Hordeum.  
 OX NCBI\_TaxId=4519;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H299, AND H801; TISSUE=LEAVES;  
 RA Petersen G., Seberg O.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Z77763; CAB01367.1; -.  
 DR EMBL: Z77762; CAB01364.1; -.  
 KW Ribosomal protein; Chloroplast.  
 FT NON\_TER 1 1  
 FT SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;  
 SQ

Query Match 22.6%; Score 7; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 P 1  
 DB 1 P 1

RESULT 13  
 P92210  
 ID P92210 PRELIMINARY; PRT; 7 AA.  
 AC P92210;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)  
 DE RIBOSOMAL PROTEIN 11 (FRAGMENT).  
 GN RPS11.  
 OS Agropyron cristatum.  
 OC Chloroplast.  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 CC Triticeae; Agropyron.  
 OX NCBI\_TaxId=4593;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H4349; TISSUE=LEAVES;  
 RA Petersen G., Seberg O.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Z77771; CAB01391.1; -.  
 KW Ribosomal protein; Chloroplast.  
 FT NON\_TER 1 1  
 FT SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;  
 SQ

Query Match 22.6%; Score 7; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 P 1  
 DB 1 P 1

RESULT 14  
 P92214  
 ID P92214 PRELIMINARY; PRT; 7 AA.  
 AC P92214;  
 DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)  
 DE RIBOSOMAL PROTEIN 11 (FRAGMENT).  
 GN RPS11.  
 OS Amblyopyrum multicum.  
 OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Trilicaceae; Amblyopyrum.  
 OX NCBI\_TaxID=4595;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H5572; TISSUE-LEAVES;  
 RA Petersen G., Seberg O.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Z77756; CAB01346.1; -.  
 KW Ribosomal protein; Chloroplast.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 22.6%; Score 7; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0;

OY 1 P 1  
 |  
 Db 1 P 1

RESULT 15  
 P92218 PRELIMINARY; PRT; 7 AA.  
 AC P92218;  
 DT 01-MAY-1997 (TREMBlrel. 03, Created)  
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
 DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)  
 DE RIBOSOMAL PROTEIN 11 (FRAGMENT).  
 GN RPS11.  
 OS Australopyrum retrofractum.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Trilicaceae; Australopyrum.  
 OX NCBI\_TaxID=4597;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H6723; TISSUE-LEAVES;  
 RA Petersen G., Seberg O.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: Z77767; CAB01379.1; -.  
 KW Ribosomal protein; Chloroplast.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 22.6%; Score 7; DB 8; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0;

OY 1 P 1  
 |  
 Db 1 P 1

Search completed: March 1, 2002, 06:55:41  
 Job time: 183 sec



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OM protein - protein search, using sw model

Run on: March 1, 2002, 06:49:03 ; Search time 23.64 Seconds

(without alignments)  
21.934 Million cell updates/sec

Title: 09-876091-2

Perfect score: 31

Sequence: 1 plg1xar 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 47201

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_1101:\*

1: /SIDSR/gcgdata/geneseq/geneseq/AA1980.DAT:\*

2: /SIDSR/gcgdata/geneseq/geneseq/AA1981.DAT:\*

3: /SIDSR/gcgdata/geneseq/geneseq/AA1982.DAT:\*

4: /SIDSR/gcgdata/geneseq/geneseq/AA1983.DAT:\*

5: /SIDSR/gcgdata/geneseq/geneseq/AA1984.DAT:\*

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22: /SIDSR/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	93.5	7	18	AAW24982
2	29	93.5	7	19	AAW51620
3	29	93.5	7	20	AAV90959
4	29	93.5	7	21	AAI13515
5	29	93.5	7	21	AAI14959
6	29	93.5	7	21	AAI12590
7	29	93.5	7	21	AAV85519
8	29	93.5	7	22	AAV65039
9	29	93.5	7	22	AAV97514
10	29	93.5	7	22	AAV74962
11	29	93.5	7	22	AAV72894

12	29	93.5	7	22	AAV62797	Peptide-lipid conj
13	29	93.5	7	22	AAV50857	Human gelatinase s
14	29	93.5	7	22	AAV50351	Human gelatinase s
15	28	90.3	7	18	AAW24983	Recombinant human
16	28	90.3	7	22	AAV74039	Synthetic collagen
17	23	74.2	6	21	AAV37325	Peptide linker #10
18	23	74.2	6	21	AAV15681	Matrix metalloprot
19	23	74.2	6	21	AAV22834	Matrix metalloprot
20	23	74.2	6	21	AAV1558	Collagenase substr
21	23	74.2	6	22	AAV67721	Amino acid sequenc
22	23	74.2	6	22	AAV67722	Amino acid sequenc
23	23	74.2	6	22	AAV3911	MMP-2 protease cle
24	23	74.2	6	22	AAV73912	MT1-MMP protease c
25	23	74.2	6	22	AAV35976	Collagenase cleava
26	23	74.2	7	22	AAV65041	Human matrix metal
27	23	74.2	7	22	AAV5135	Gelatinase recogni
28	23	74.2	7	22	AAV35980	Gelatinase cleavab
29	22	71.0	7	22	AAV65036	Human matrix metal
30	22	71.0	7	22	AAV35977	Collagenase cleava
31	21	67.7	4	4	AAV30449	Substrate for coll
32	21	67.7	4	4	AAV30450	Substrate for coll
33	21	67.7	4	19	AAV51622	Peptide-lipid conj
34	21	67.7	4	22	AAV62798	Sequence of synthe
35	21	67.7	6	5	AAV40806	Sequence of synthe
36	21	67.7	6	5	AAV40807	3-methylcholanthre
37	21	67.7	6	18	AAV74602	Recombinant human
38	21	67.7	6	18	AAV24981	Matrix metalloprot
39	21	67.7	6	19	AAV52139	Thiopeptolide subs
40	21	67.7	6	21	AAV23852	Thiopeptolide subs
41	21	67.7	6	21	AAV1359	Thiopeptolide subs
42	21	67.7	6	22	AAV70300	Thiopeptolide amin
43	21	67.7	6	22	AAV74620	Thiopeptolide. Un
44	21	67.7	6	22	AAV68684	Matrix metalloprot
45	21	67.7	6	22	AAV60147	

#### ALIGNMENTS

RESULT 1	
AAW24982	standard; peptide; 7 AA.
AAW24982	
03-DEC-1997	(first entry)
Recombinant human gelatinase fluorogenic peptide substrate #1.	
Catalytic domain; human; gelatinase; matrix metalloprotease; propeptide;	
hemopoietic; fibronectin; vector; recombinant; deletion; hermia; joint;	
vertebral disc; dermal ulcer; scar tissue.	
Synthetic.	
Key	Location/Qualifiers
Modified-site	1 /note="Mca-Pro"
Modified-site	5 /label="OTHER
Modified-site	7 /note="Dpa"
Modified-site	/note="amidated C-terminus"
US5646027-A.	
08-JUL-1997.	
08-SEP-1994.	94US-0303270.
08-SEP-1994.	94US-0303270.
(WARN ) WARNER LAMBERT CO.	

XX Hupe DJ, Johnson LL, Ye Q;  
XX WPI: 1997-362935/33.  
XX Production of recombinant human gelatinase catalytic domain protein  
XX - especially using vector containing new synthetic coding sequence  
XX  
XX Example 4: Column 11: 21pp: English.  
XX  
XX This peptide is a substrate for a novel recombinant catalytic domain of  
XX the human 72 kD gelatinase, a member of the matrix metalloproteinase  
XX family, lacking its propeptide, C-terminal hemopexin-like domain or  
XX fibronectin-like insert (AAW24980). The catalytic domain protein is  
XX useful for treating herniated vertebral discs, treating dermal ulcers,  
XX modifying scar tissue formation and treating joint diseases.  
XX  
XX Sequence 7 AA:  
SQ

Query Match 93.5%; Score 29; DB 18; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.3e+05; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 plgixar 7  
Db 1 plgixar 7

RESULT 2  
AAW51620  
ID AAW51620 standard; peptide: 7 AA.  
XX  
XX AAW51620:  
XX  
XX 03-SEP-1998 (first entry)  
XX  
XX Peptide conjugated to lipid for use in liposomal drug delivery.  
XX  
XX Liposome; conjugate; drug delivery; peptidase-secreting cell;  
XX tumour; diagnosis; therapy.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
XX Modified-site 5 /note= "Diphenylalanine"  
XX Modified-site 7 /note= "C-terminal amide"  
XX  
XX W09816240-A1.  
XX  
XX 23-APR-1998.  
XX  
XX 15-OCT-1997; 97WO-US18538.  
XX  
XX 15-OCT-1996; 96US-0027544.  
XX  
XX (LIP0 ) LIPOSOME CO INC.  
XX  
XX Ali S, Cabralilly D, Erukulla RK, Franklin JC;  
XX Janoff AS, Meers PR, Pak C;  
XX  
XX WPI: 1998-261025/23.  
XX  
XX New peptide-lipid conjugates are incorporated into liposome(s) - to  
XX selectively destabilise the liposome(s) in the vicinity of target  
XX peptidase-secreting cells, e.g., tumour cells; useful in diagnosis  
XX and therapy  
XX  
XX Claim 8; Page 33; 55pp: English.  
XX  
XX The invention relates to peptide-lipid conjugates and their use in

CC the preparation of liposomes which are predisposed to degradation in the  
CC presence of peptidase-secreting cells and hence are targeted to these  
CC cells. The liposomes can be used to treat mammalian diseases, disorders  
CC and conditions, e.g. tumours, microbial infections and inflammation. The  
CC liposomes allow selective delivery of an active agent to desired cells.  
CC The liposomes are stable when the peptide remains conjugated to the  
CC lipid. However, once the peptide portion of the conjugate is cleaved  
CC from the lipid, by the action of cell-secreted peptidases, the liposomes  
CC destabilise and release their contents in the vicinity of, or into, the  
CC secreting cells. The liposomes can thus be used to treat conditions  
CC characterised by the occurrence of peptidase-secreting cells. For  
CC example, the breast cancer cell line MCF-7 is known to secrete elastase,  
CC the levels of which are inversely correlated to overall survival in  
CC breast cancer patients. The present sequence represents a specifically  
CC claimed peptide which forms part of the peptide-lipid conjugate.  
XX  
XX Sequence 7 AA:  
SQ

Query Match 93.5%; Score 29; DB 19; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.3e+05; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 plgixar 7  
Db 1 plgixar 7

RESULT 3  
AAV90959  
ID AAV90959 standard; peptide: 7 AA.  
XX  
XX AAV90959:  
XX  
XX 31-AUG-2000 (first entry)  
XX  
XX Human matrix metalloproteinase 2 peptide.  
XX  
XX Human; matrix metalloproteinase 2; MMP-2; therapeutic; prophylactic;  
XX glomerulopathy; collagenase IV; inhibitor; nephritis; diabetes.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Modified-site 1 /note= "Pro is N-terminally modified to MOCAC-Pro"  
XX Modified-site 5 /note= "X is A2Pr(Dnp)"  
XX Modified-site 7 /note= "amidated"  
XX  
XX W09904780-A1.  
XX  
XX 04-FEB-1999.  
XX  
XX 17-JUL-1998; 98WO-JP03226.  
XX  
XX 22-JUL-1997; 97JP-0195414.  
XX  
XX (SHIO ) SHIONOGI & CO LTD.  
XX  
XX Kurihara H, Watanabe F, Tamura Y, Sinosaki T;  
XX  
XX WPI: 1999-142583/12.  
XX  
XX Agent for treatment of glomerulopathy e.g. due to nephritis or diabetes  
XX - comprises new or known sulphonamide compound  
XX  
XX Disclosure; Page 63; 102pp: Japanese.  
XX  
XX The present invention describes an agent for the treatment or prevention  
XX of glomerulopathy. The agents of the present invention are collagenase IV  
XX inhibitors and are useful for the treatment and prevention of

CC glomerulopathy (e.g. due to nephritis or diabetes). The present sequence  
 CC represents a human matrix metalloproteinase 2 (MMP-2) which is used in  
 CC the exemplification of the present invention.

XX Sequence 7 AA:

Query Match 93.5%; Score 29; DB 20; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 plglxar 7  
 |||||  
 Db 1 plglxar 7

#### RESULT 4

AAB13515  
 ID AAB13515 standard; peptide; 7 AA.

AC AAB13515;

DT 06-MAR-2001 (first entry)

DE Human procollagen C-proteinase inhibition assay substrate #4.

XX Human; procollagen C-proteinase; PCP; bone morphogenetic protein-1;  
 KM BMP-1; collagen deposition; fibrotic disease; pericentral fibrosis;  
 KM interstitial pulmonary fibrosis; Symmers' fibrosis; kidney fibrosis;  
 KM perimuscular fibrosis; endocardial sclerosis; hepatitis; arthritis;  
 KM acute respiratory distress syndrome; cystic fibrosis; surgical adhesion;  
 KM scleroderma; restenosis.

OS Synthetic.

FT Key Location/Qualifiers

FT Modified-site 1 /note= "modified by MCA"

FT Misc-difference 5 /note= "DPA"

FT Modified-site 7 /note= "C-terminal amide"

FT WO200034313-A1.

PD 15-JUN-2000.

PF 06-DEC-1999; 99WO-EP09519.

PR 10-DEC-1998; 98US-0111661.

PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.

PI Dankwardt SM, Van Wart HE, Walker KM;

DR WPI: 2000-431271/37.

XX New peptidic hydroxamic acid derivatives useful for treating fibrotic  
 PT diseases e.g. acute respiratory distress syndrome -

XX Example 14; Page 62; 78pp; English.

XX The present sequence is a peptide substrate which was used in an assay to  
 CC determine the efficiency of human procollagen C-proteinase (PCP, also  
 CC known as bone morphogenetic protein-1 or BMP-1) inhibitory compounds. PCP  
 CC is involved in the deposition of collagen. PCP inhibitors are useful as  
 CC they prevent excessive collagen deposition, and can be used to treat  
 CC fibrotic diseases such as interstitial pulmonary fibrosis, pericentral  
 CC fibrosis, Symmers' fibrosis, perimuscular fibrosis, kidney fibrosis,  
 CC endocardial sclerosis, hepatitis, acute respiratory distress syndrome,  
 CC arthritis, cystic fibrosis, surgical adhesions, tendon surgery, corneal  
 CC scarring, scleroderma, chronic allograft rejection, haemodialysis shunt  
 CC fibrosis and restenosis.

XX Sequence 7 AA:

Query Match 93.5%; Score 29; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 plglxar 7  
 |||||  
 Db 1 plglxar 7

#### RESULT 5

AAB14959  
 ID AAB14959 standard; peptide; 7 AA.

AC AAB14959;

DT 29-NOV-2000 (first entry)

DE Fluorogenic substrate used to assay matrix metalloproteinases.

XX Matrix metalloproteinases; MMP; fluorescence; neoplasm;  
 KM atherosclerosis; inflammatory disease.

OS Synthetic.

FT Key Location/Qualifiers

FT Modified-site 1 /note= "Fluorogenic N-terminal Mca"

FT Misc-difference 5 /note= "Given in specification as Dpa"

FT WO200040564-A1.

PD 13-JUL-2000.

PF 30-NOV-1999; 99WO-US28339.

PR 31-DEC-1998; 98US-0224549.

PA (AVET ) AVENTIS PHARM INC.

PI Marshawsky A, Janusz MJ, Flynn GA;

DR WPI: 2000-465936/40.

XX New benzazepine derivatives, useful for treatment of neoplastic states,  
 PT atherosclerosis and inflammatory diseases such as emphysema, chronic  
 PT bronchitis and asthma, are matrix metalloproteinase inhibitors

XX Example A; Page 64; 108pp; English.

XX The present invention relates to benzolactam derivatives used as  
 CC inhibitors of matrix metalloproteinase. The benzolactam derivatives may  
 CC be used for treatment of neoplastic states such as leukemias, carcinomas,  
 CC adenocarcinomas, sarcomas, melanomas and mixed neoplasias,  
 CC atherosclerosis, chronic inflammatory disease, rheumatoid arthritis,  
 CC osteoarthritis, cardiovascular disorders, corneal ulceration, dental  
 CC diseases and neurological disorders such as multiple sclerosis. The  
 CC present sequence is a fluorogenic substrate used to assay the activated  
 CC matrix metalloproteinases 1, 3 and 12. The matrix metalloproteinases  
 CC cleave the substrate at the Gly-Leu peptide bond, causing an increase  
 CC in fluorescence.

XX Sequence 7 AA:

Query Match 93.5%; Score 29; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgixar 7  
 |||||  
 Db 1 plgixar 7

RESULT 6  
 AAB12590  
 ID AAB12590 standard; Peptide: 7 AA.  
 XX  
 AC AAB12590;

DT 09-NOV-2000 (first entry)

DE Inhibition of collagenase activity assay substrate SEQ ID NO:8.

XX Human; procollagen C-protein; PCP: bone morphogenetic protein 1; BMP-1;  
 KW sulphonomide hydroxamate; inhibitor; cytosolic; hepatotropic;  
 KW antiinflammatory; virucide; antiarthritic; vasotrophic; vulnerary;  
 KW ophthalmological; interstitial collagen; interstitial pulmonary fibrosis;  
 KW Symmer's fibrosis; perimuscular fibrosis; kidney fibrosis; hepatitis;  
 KW liver fibrosis; idiopathic pulmonary fibrosis; endocardial sclerosis;  
 KW acute respiratory distress syndrome; arthritis; cystic fibrosis;  
 KW tendon surgery; surgical adhesion; corneal scarring; restenosis;  
 KM  
 XX Homo sapiens.

OS Key Location/Qualifiers

FT Modified-site 1 /note= "Pro is N-terminally modified to MCA-Pro"

FT Modified-site 5 /note= "X is DPA, which is not defined further in the specification"

FT Modified-site 7 /note= "amidated"

FT WO200037436-A1.

PN 29-JUN-2000.

PD 14-DEC-1999; 99WO-EP09920.

PF 22-DEC-1998; 98US-0113311.

PR 03-AUG-1999; 99US-0147053.

XX (HOEF ) HOFFMANN LA ROCHE & CO AG F.

XX Billideau RJ, Broka CA, Campbell JA, Chen JJ, Dankwardt SM;

PI Delaet N, Robinson LA, Walker KAM;

XX WPI; 2000-514524/46.

PT New aryl sulfonamide hydroxamate derivatives useful for treatment of e.g. fibrosis, arthritis and hepatitis, are procollagen C-proteinase inhibitors.

PS Example 22; Page 109; 133pp; English.

XX The present invention describes aryl sulphonomide hydroxamate derivatives. Aryl sulphonomide hydroxamate derivatives can be used for the treatment of disease treatable by procollagen C-proteinase inhibitors (especially interstitial collagens), e.g. interstitial pulmonary fibrosis, Symmer's fibrosis, perimuscular fibrosis, kidney or liver fibrosis, idiopathic pulmonary fibrosis, endocardial sclerosis, hepatitis, acute respiratory distress syndrome, arthritis, cystic fibrosis, tendon surgery, surgical adhesions, corneal scarring and restenosis. They have cytosolic, hepatotropic, antiinflammatory, virucide, antiarthritic, vasotropic, vulnerary and ophthalmological activities. The present sequence represents a peptide substrate used in an assay for the inhibition of collagenase activity, which is used in an example from the present invention.

CC Sequence 7 AA;

Query Match 93.5%; Score 29; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgixar 7  
 |||||  
 Db 1 plgixar 7

RESULT 7  
 AAY85519  
 ID AAY85519 standard; peptide: 7 AA.  
 XX  
 AC AAY85519;

DT 23-JUN-2000 (first entry)

DE Substrate for template-ligand conjugate.

XX Template ligand conjugate; triple helix coil; enzyme purification;  
 KW molecular modelling.

XX Synthetic.

OS Key Location/Qualifiers

FT Modified-site 5 /label= Dpa

FT Modified-site 7 /note= "hydroxyproline"

FT Modified-site 7 /note= "C-terminal amide"

FT WO200012538-A1.

PN 09-MAR-2000.

PD 23-AUG-1999; 99WO-US19367.

PF 31-AUG-1998; 98US-0144419.

PR (CHEN/) CHEN J.

XX (YEH/) YEH L.

PI Chen J, Yeh L;

XX WPI; 2000-246726/21.

PT New triple helix coil template having biologically active ligand, useful for substrate based drug screening tool comprising increased target specificity and affinity.

PS Example 2; Page 14; 29pp; English.

XX The invention relates to a template ligand conjugate (I) comprising a template made of three cross linked polypeptide chains which each contain CC tripeptide or hexapeptide repeat sequences aligned to form a triple helix CC coil and a first biologically active ligand attached to the template via CC covalent bonding with one of the three polypeptide chains. (I) is useful for presenting one or more biologically active ligands to a target, as a CC substrate based drug screening tool in lieu of traditional linear peptide CC-based combinatorial methods and can be used in highly specific and CC efficient columns for the purification of enzymes. (I) can be used to CC assay a sample, such as serum or synovial fluid, for the presence of a CC specific enzyme. (I) can also be used to target an enzyme, an effector or CC receptor e.g. to treat a disease that is induced or exacerbated by one or CC more enzymes. The conjugate (I) has a well defined three dimensional CC structure and a biologically active ligand attached to it may be studied CC immediately using molecular modelling. (I) also provides a greater CC surface region for chemical modifications to increase target specificity CC and affinity through multi domain binding and to alter any undesirable CC chemical properties. (I) enables one to reduce the conformational CC flexibility or entropy of the biologically active ligand in a selective CC manner. The present sequence represents a substrate for template-ligand



CC conjugate.  
XX  
SQ Sequence 7 AA;

Query Match 93.5%; Score 29; DB 21; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 plgxar 7  
1111111  
Db 1 plgxar 7

RESULT 8  
AAG65039  
ID AAG65039 standard; peptide: 7 AA.  
XX  
AC AAG65039;  
XX  
DT 09-OCr-2001 (first entry)  
XX  
DE Human matrix metalloproteinase MMP-7 substrate peptide.  
XX  
KM Chemical sensor system; microjet; indicator chemistry; ligand analysis;  
KM biomedicine; environmental monitoring; bio warfare.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT Modified-site /note= "modified by Mca"  
FT Modified-site 7 /label= OTHER  
FT Modified-site /note= "C-terminal amide"  
XX  
PN WO200157494-A2.  
XX  
PD 09-AUG-2001.  
XX  
PE 17-JAN-2001; 2001WO-US01553.  
XX  
PR 20-JAN-2000; 2000US-0177105.  
PR 09-NOV-2000; 2000US-0709047.  
XX  
PA (RECC ) UNIV CALIFORNIA.  
XX  
PI Brown SB, Colston BW, Langry K, Milanovich FP, Simon J, Cox WR;  
PI Hayes DJ;  
XX  
DR WPI: 2001-488913/53.  
XX  
PS Disclosure; Page 13; 31pp; English.  
XX  
CC The present invention relates to a method of producing a chemical sensor,  
CC involving the use of microjet technology to print one or more indicator  
CC chemistries on an optically accessible surface. This is useful for  
CC producing a chemical sensor useful for detecting and/or analysing a  
CC sample in a fluid or airborne medium, for monitoring hazardous materials  
CC such as heavy metals, hydrocarbons and chlorinated hydrocarbons in both  
CC ground water and soil of contaminated sites, for making accurate  
CC dosimetry measurements of hazardous materials, such as carcinogens or  
CC mutagens present in hostile or potentially hostile environments. The  
CC sensor systems can be implemented in assembly line type configurations  
CC for quality and process control type applications, e.g. measurements of  
CC gases emitted from fruits and vegetables and detection of contaminants in  
CC soft drink or bottled water solutions. The systems are used for detection

CC of airborne or water-based chemical and bio warfare agents such  
CC as anthrax and are suitable for measuring multiple constituents in a  
CC small sample volume. The present sequence is a substrate for a matrix  
CC metalloproteinase described in the exemplification of the invention.  
XX  
SQ Sequence 7 AA;

Query Match 93.5%; Score 29; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgxar 7  
1111111  
Db 1 plgxar 7

RESULT 9  
AAB97514  
ID AAB97514 standard; peptide: 7 AA.  
XX  
AC AAB97514;  
XX  
DT 14-AUG-2001 (first entry)  
XX  
DE Substituted phosphinate based peptide derivative #2.  
XX  
KM Phosphinate peptide derivative; metabolic bone disease; osteoporosis;  
KM bone metastasis; cancer; bone resorption; metalloproteinase.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT Cleavage-site /note= "modified by (7-methoxycoumarin-4-yl)acetyl"  
FT Cleavage-site 3..4 /note= "cleaved by MMP-1 and MMP-14"  
FT Modified-site 5 /label= OTHER  
FT Modified-site /note= "(2',4'-dinitrophenyl)-L-2,3-diaminopropionyl"  
FT Modified-site 7 /label= OTHER  
FT Modified-site /note= "C-terminal amide"  
XX  
PN WO200125264-A2.  
XX  
PD 12-APR-2001.  
XX  
PE 19-SEP-2000; 2000WO-EP09173.  
XX  
PR 23-SEP-1999; 99GB-0022577.  
XX  
PA (OSTE-) OSTEOPRO AS.  
XX  
PI Buchardt J, Foged NT, Meldal M, Delaisse J, Engsig M, Ferreras M;  
PI Karsdal M, Ovejero MDC, Schiodt CB, Winding B;  
XX  
DR WPI: 2001-343189/36.  
XX  
PS Disclosure; Page 29; 149pp; English.  
XX  
CC Use of new and known substituted phosphinate based peptide derivatives  
CC for treating metabolic bone diseases e.g. osteoporosis or bone  
CC metastasis -  
XX  
CC The present invention describes the use of substituted phosphinate based  
CC peptide derivatives for the treatment of metabolic bone diseases,  
CC particularly those related to metalloproteinases. Bone diseases to be  
CC treated include bone metastases (due to tumours) and osteoporosis. The  
CC present sequence is a peptide described in the exemplification of the  
CC invention.

SQ Sequence 7 AA;  
 Query Match 93.5%; Score 29; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 p1g1xar 7  
 1111111  
 1 p1g1xar 7  
 Db 1 p1g1xar 7  
 RESULT 10  
 AAB74962  
 ID AAB74962 standard; Peptide: 7 AA.  
 AC AAB74962;  
 XX  
 DT 11-JUL-2001 (first entry)  
 XX  
 DE Coumarin-labelled peptide matrix metalloproteinase substrate.  
 XX  
 KW Human; MT1-MMP; MMP1; collagenase 1; MMP2; gelatinase A; stromelysin;  
 KW arylsulfonylamido-substituted hydroxamic acid derivative; MMP inhibitor;  
 KW matrix degrading metalloproteinase; antiinflammatory; antirheumatic;  
 KW antiarthritic; osteopathic; cytostatic; hyperproliferative disease;  
 KW asthma; chronic obstructive pulmonary disease; COPD; tumour; metastasis;  
 KW inflammatory condition; rheumatoid arthritis; osteoarthritis;  
 KW pulmonary disease; emphysema.  
 KW  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT Modified-site 5 /label= Pro is N-terminally labelled with MCA  
 FT Modified-site 7 /note= "given as Dpa in the specification"  
 FT Modified-site 7 /note= "amidated"  
 FT  
 FT  
 FT  
 PN WO200110827-A1.  
 XX  
 PD 15-FEB-2001.  
 XX  
 PF 07-AUG-2000; 2000WO-EP07641.  
 XX  
 PR 09-AUG-1999; 99GB-0018684.  
 XX  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
 XX  
 PI Breitenstein W, Hayakawa K, Iwasaki G, Kanazawa T, Kasaoka T;  
 PI Koizumi S, Matsunaga S, Nakajima M, Sakaki J;  
 XX  
 DR WPI: 2001-281265/29.  
 XX  
 XX  
 PT New arylsulfonylamido-substituted hydroxamic acid derivatives, useful for  
 PT treating inflammatory conditions, rheumatoid arthritis, osteoarthritis,  
 PT tumors and pulmonary diseases, are matrix metalloproteinase inhibitors  
 PT  
 PT  
 PT  
 PS Disclosure; Page 11; 98pp; English.  
 XX  
 CC The present invention describes arylsulfonylamido-substituted hydroxamic  
 CC acid derivatives (I). Also described are: (1) a pharmaceutical  
 CC composition comprising (I); and (2) preparation of (I). (I) has  
 CC antiinflammatory, antirheumatic, antiarthritic, osteopathic and  
 CC cytostatic activities, and can be used as an inhibitor of matrix  
 CC degrading metalloproteinase (MMP). (I) is useful for treating conditions  
 CC or diseases associated with MMP2 in warm blooded animals including  
 CC humans, such as hyperproliferative diseases, asthma, chronic obstructive  
 CC pulmonary disease (COPD) and tumours. (1) and pharmaceutical compositions  
 CC comprising (1) are useful in chemotherapy of tumours, COPD and asthma.

CC (1) is also useful for treating inflammatory conditions, rheumatoid  
 CC arthritis, osteoarthritis, tumours (tumour growth, metastasis,  
 CC progression or invasion), and pulmonary diseases (e.g. emphysema). The  
 CC present sequence represents a coumarin-labelled peptide matrix  
 CC metalloproteinase substrate, which is given in the exemplification of  
 CC the present invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 93.5%; Score 29; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 p1g1xar 7  
 1111111  
 1 p1g1xar 7  
 Db 1 p1g1xar 7  
 RESULT 11  
 AAB72894  
 ID AAB72894 standard; peptide: 7 AA.  
 XX  
 AC AAB72894;  
 XX  
 DT 11-MAY-2001 (first entry)  
 XX  
 DE Human gelatinase inhibition assay substrate peptide.  
 XX  
 KW Metalloproteinase inhibitor; inflammation; cancer; autoimmune disease;  
 KW neurodegenerative disorder; cardiovascular disease; repolysin.  
 KW  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT Modified-site 5 /label= OTHER  
 FT Modified-site 7 /note= "modified by MCA"  
 FT Modified-site 5 /label= OTHER  
 FT Modified-site 7 /note= "Dpa"  
 FT Modified-site 7 /label= OTHER  
 FT Modified-site 7 /note= "C-terminal amide"  
 FT  
 FT  
 FT  
 PN WO200112611-A1.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 03-AUG-2000; 2000WO-IB01090.  
 XX  
 PR 12-AUG-1999; 99US-0148547.  
 XX  
 PA (PFI2 ) PFIZER PROD INC.  
 PA  
 PI Blagg J;  
 XX  
 DR WPI: 2001-218336/22.  
 XX  
 XX  
 PT Novel pyrimidine-2,4,6-trione metalloproteinase inhibitors, useful for  
 PT treating e.g. inflammation, cancer, arthritis, auto-immune disorders,  
 PT neurodegenerative disorders, stroke or AIDS  
 PT  
 PT  
 PS Disclosure; Page 25; 47pp; English.  
 XX  
 CC The present invention provides inhibitors of pyrimidine-2,4,6-trione  
 CC metalloproteinases, particularly inhibitors of matrix metalloproteinases  
 CC and repolysin. These are useful in the treatment of diseases such as  
 CC cancer, neurodegenerative disorders such as Alzheimer's, Parkinson's and  
 CC Huntington's diseases, inflammation, including arthritis, inflammatory  
 CC bowel disease, asthma and Crohn's disease, cardiovascular diseases such  
 CC as congestive heart failure and myocardial infarction, and autoimmune  
 CC diseases, including diabetes, allergies and multiple sclerosis. The

CC present sequence is a peptide substrate used to demonstrate the action of  
CC the inhibitors of the invention.

SO Sequence 7 AA;

Query Match 93.5%; Score 29; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgixar 7  
1111111  
Db 1 plgixar 7

#### RESULT 12

AAB62797  
ID AAB62797 standard; peptide: 7 AA.

AC AAB62797;

DT 03-APR-2001 (first entry)

XX Peptide-lipid conjugate peptide #12.

XX Peptide-lipid conjugate; liposome; liposomal drug delivery; cancer;

KM peptidase-secreting cell; phosphatidylethanolamine;

XX inflammatory disorder; neuropathy.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 5

FT /label= OTHER

FT /note= "N-3-(2,4-dinitrophenyl)-L-2,3-diaminopropionyl"

FT Modified-site 7

FT /label= OTHER

FT /note= "C-terminal amide"

XX WO200100247-A1.

XX 04-JAN-2001.

XX 13-JUN-2000; 2000WO-US16248.

XX 29-JUN-1999; 99US-0343650.

XX (LIPPO ) LIPOSOME CO INC.

XX Meers P, Pak C, Ali S, Janoff A, Franklin JC, Erkulalla R;

XX Cabral-Lally D, Ahl P;

XX WPI; 2001-122976/13.

XX LIPosomal drug delivery for treating cancer, inflammatory, genetic

PT disorders and microbial infections, involves administering liposomes

PT comprising peptide-lipid conjugates -

XX Claim 6; Page 61; 107pp; English.

XX The present invention describes a method of administering the contents of

CC a liposome to a cell by administering a liposome containing a

CC peptide-lipid conjugate where the peptide is cleavable by a peptidase

CC and the lipid is a phosphatidylethanolamine. This can be used in

CC liposomal drug delivery, for example in the treatment of cancer,

CC inflammatory disorders and neuropathies.

XX Sequence 7 AA;

SO Query Match 93.5%; Score 29; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgixar 7  
1111111  
Db 1 plgixar 7

RESULT 13  
AAB50857  
ID AAB50857 standard; peptide: 7 AA.

AC AAB50857;

DT 16-MAR-2001 (first entry)

XX Human gelatinase substrate peptide.

XX Human gelatinase; MMP-2; immunosuppressive; antiallergic; cytostatic;

KM osteopathic; immunomodulator; vasotropic; dermatological;

KM antiarteriosclerotic; cardiant; cerebroprotective; anticonvulsant;

KM antimigraine; antidepressant; analgesic; ophthalmological; vulnerary;

KM anti-HIV; antibacterial; anti-Parkinsonian; antidiabetic;

KM 3-(arylsulfonylamino)-tetrahydrofuran-3-carboxylic acid hydroxamide;

KM matrix metalloproteinase; MMP.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1

FT /note= "Mca-Pro"

FT Modified-site 5

FT /note= "given as dpa, not further defined"

FT Modified-site 7

FT /note= "C-terminal amide"

XX WO200073294-A2.

XX 07-DEC-2000.

XX 15-MAY-2000; 2000WO-IB00646.

XX 28-MAY-1999; 99US-0136677.

XX (PEI2 ) PFIZER PROD INC.

XX Reiter LA;

XX WPI; 2001-091061/10.

XX New 3-(arylsulfonylamino)-tetrahydrofuran-3-carboxylic acid hydroxamide

PT compounds useful for treating e.g. inflammation, cancer and autoimmune,

PT neurodegenerative and cardiovascular disorders -

XX Disclosure; Page 26; 46pp; English.

XX The present sequence was used as a substrate in a matrix

CC metalloproteinase (MMP) assay. The invention relates to novel

CC 3-(arylsulfonylamino)-tetrahydrofuran-3-carboxylic acid hydroxamide

CC compounds and their salts. These are useful for treating arthritis,

CC inflammatory bowel disease, Crohn's disease, emphysema, chronic

CC obstructive pulmonary disease, Alzheimer's disease, organ transplant

CC toxicity, cachexia, allergic reactions, allergic contact

CC hypersensitivity, cancer, tissue ulceration, restenosis, periodontal

CC disease, epidermolysis bullosa, osteoporosis, loosening of artificial

CC joint implants, atherosclerosis, aortic aneurysm, congestive heart

CC failure, myocardial infarction, stroke, cerebral ischemia, head trauma,

CC spinal cord injury, neurodegenerative disorders, autoimmune disorders,

CC Huntington's disease, Parkinson's disease, migraine, depression,

CC peripheral neuropathy, pain, cerebral amyloid angiopathy, neurotrophic or

CC cognition enhancement, amyotrophic lateral sclerosis, multiple sclerosis,

CC ocular angiogenesis, corneal injury, macular degeneration, abnormal wound

CC healing, burns, diabetes, tumour invasion, tumour growth, tumour

CC metastasis, corneal scarring, scleritis, AIDS, sepsis and septic shock

CC in a mammal.

```

XX SQ Sequence 7 AA;
Query Match 93.5%; Score 29; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 p1glxar 7
Db 1 p1glxar 7

RESULT 14
AAB50351
ID AAB50351 standard; peptide; 7 AA.
AC AAB50351;
XX 09-MAR-2001 (first entry)
DE Human gelatinase substrate.
XX Human gelatinase: MMP-2; antiarthritic; gastrointestinal; respiratory;
KW neuroprotective; immunosuppressive; anabolic; antiallergic; antiulcer;
KW cardiatic; dermatological; vasotropic; dermatological; cerebroprotective;
KW antiparkinsonian; analgesic; antidepressant; anticonvulsant; cyrostatic;
KW ophthalmological; vulnery; anti-HIV; antibacterial; analgesic;
KW antidiabetic; nootropic; antiarteriosclerotic;
KW 3-(Sulfonylamino)-tetrahydropyran-3-carboxylic acid hydroxamide.
XX Unidentified.
OS Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1 /note= "Mca-Pro"
FT Modified-site 5 /note= "Dpa (not further defined)"
FT Modified-site 7 /note= "C-terminal amide"
XX WO200073295-A1.
XX 07-DEC-2000.
XX 15-MAY-2000; 2000WO-IB00647.
XX 28-MAY-1999; 99US-0136530.
XX (Pfizer ) Pfizer Prod Inc.
XX Reiter LA.
XX WPI; 2001-102326/11.
XX New 3-(sulfonylamino)-tetrahydropyran-3-carboxylic acid hydroxamide
PT derivatives are metalloproteinase inhibitors used for treating e.g.
PT inflammation, cancer, allergy and autoimmune disease
XX Disclosure; Page 26; 51pp; English.
XX The present sequence was used to analyse human gelatinase (MMP-2)
CC inhibition. 3-(Sulfonylamino)-tetrahydropyran-3-carboxylic acid
CC hydroxamide derivatives act as inhibitors and may be used for treating
CC arthritis. Inflammatory bowel disease, Crohn's disease, emphysema,
CC chronic obstructive pulmonary disease, Alzheimer's disease, organ
CC transplant toxicity, cachexia, allergic reactions, allergic contact
CC hypersensitivity, cancer, tissue ulceration, restenosis, periodontal
CC disease, epidermolysis bullosa, osteoporosis, loosening of artificial
CC joint implants, atherosclerosis, aortic aneurysm, congestive heart
CC failure, myocardial infarction, stroke, cerebral ischemia, head trauma,
CC spinal cord injury, neurodegenerative disorders, autoimmune disorders,

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CC Huntington's disease, Parkinson's disease, migraine, depression,
CC peripheral neuropathy, pain, cerebral amyloid angiopathy, nootropic or
CC cognition enhancement, amyotrophic lateral sclerosis, multiple sclerosis,
CC ocular angiogenesis, corneal injury, muscular degeneration, abnormal
CC wound healing, burns, diabetes, tumour invasion, tumour growth, tumour
CC metastasis, corneal scarring, scleritis, AIDS, sepsis and septic shock.
XX SQ Sequence 7 AA;
Query Match 93.5%; Score 29; DB 22; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 p1glxar 7
Db 1 p1glxar 7

RESULT 15
AAW24983
ID AAW24983 standard; peptide; 7 AA.
AC AAW24983;
XX 03-DEC-1997 (first entry)
DE Recombinant human gelatinase fluorogenic peptide substrate #2.
XX Catalytic domain; human; gelatinase; matrix metalloprotease; propeptide;
KW hemopepin; fibronectin; vector; recombinant; deletion; hernia; joint;
KW vertebral disc; dermal ulcer; scar tissue.
XX Synthetic.
OS Key Location/Qualifiers
FH Modified-site 1 /note= "Dmp-Pro"
FT Misc-difference 7 /note= "D-form residue and amidated C-terminus"
XX US5646027-A.
XX 08-JUL-1997.
XX 08-SEP-1994; 94US-0303270.
XX 08-SEP-1994; 94US-0303270.
XX (WARN ) WARNER LAMBERT CO.
XX Hupe DJ, Johnson LL, Ye Q;
XX WPI; 1997-362935/33.
XX Production of recombinant human gelatinase catalytic domain protein
PT - especially using vector containing new synthetic coding sequence
XX Example 4; Column 12; 21pp; English.
XX This peptide is a substrate for a novel recombinant catalytic domain of
CC the human 72 kD gelatinase, a member of the matrix metalloprotease
CC family, lacking its propeptide, C-terminal hemopepin-like domain or
CC fibronectin-like insert (AAW24980). The catalytic domain protein is
CC useful for treating herniated vertebral discs, treating dermal ulcers,
CC modifying scar tissue formation and treating joint diseases.
XX SQ Sequence 7 AA;
Query Match 90.3%; Score 28; DB 18; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.3e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 plglxar 7  
| | | | |  
Db 1 plglwar 7

Search completed: March 1, 2002, 06:52:36  
Job time: 213 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2002, 06:52:08 ; Search time 90.58 Seconds  
(without alignments)  
21.457 Million cell updates/sec

Title: 09-876091-2  
Perfect score: 31  
Sequence: 1 p1g1xar 7

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 117338

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

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2: /cgn2\_6/ptodata/2/paa/US06\_COMB.pep: \*  
3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep: \*  
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7: /cgn2\_6/ptodata/2/paa/US083\_COMB.pep: \*  
8: /cgn2\_6/ptodata/2/paa/US084\_COMB.pep: \*  
9: /cgn2\_6/ptodata/2/paa/US085\_COMB.pep: \*  
10: /cgn2\_6/ptodata/2/paa/US086\_COMB.pep: \*  
11: /cgn2\_6/ptodata/2/paa/US087\_COMB.pep: \*  
12: /cgn2\_6/ptodata/2/paa/US088\_COMB.pep: \*  
13: /cgn2\_6/ptodata/2/paa/US089\_COMB.pep: \*  
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22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep: \*  
23: /cgn2\_6/ptodata/2/paa/US099\_COMB.pep: \*  
24: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	96.8	7	21	US-09-753-078-18
2	29	93.5	7	15	US-09-168-010-14
3	29	93.5	7	16	US-09-248-158-1
4	29	93.5	7	17	US-09-343-650-14
5	29	93.5	7	18	US-09-464-908A-1
6	29	93.5	7	21	US-09-753-078-8
7	29	93.5	7	22	US-09-808-832-209
8	28	90.3	7	21	US-09-753-078-7
9	28	90.3	7	21	US-09-753-078-16

10	24	77.4	7	21	US-09-753-078-6	Sequence 6, Appl1
11	23	74.2	6	13	US-08-909-601-34	Sequence 34, Appl1
12	23	74.2	6	13	US-08-909-601-34	Sequence 34, Appl1
13	23	74.2	6	13	US-08-909-607-34	Sequence 34, Appl1
14	23	74.2	6	18	US-09-496-231A-30	Sequence 30, Appl1
15	23	74.2	6	19	US-09-561-005-24	Sequence 24, Appl1
16	23	74.2	6	19	US-09-561-108-24	Sequence 24, Appl1
17	23	74.2	6	19	US-09-561-199-24	Sequence 24, Appl1
18	23	74.2	6	19	US-09-561-500-24	Sequence 24, Appl1
19	23	74.2	6	19	US-09-561-526-24	Sequence 24, Appl1
20	23	74.2	6	19	US-09-562-245-24	Sequence 24, Appl1
21	23	74.2	6	20	US-09-639-667-7	Sequence 7, Appl1
22	23	74.2	6	20	US-09-640-198-9	Sequence 9, Appl1
23	23	74.2	6	20	US-09-640-198-11	Sequence 11, Appl1
24	23	74.2	7	21	PCT-US00-29080-3	Sequence 3, Appl1
25	23	74.2	7	21	US-09-704-251-6	Sequence 6, Appl1
26	23	74.2	7	21	US-09-704-251-35	Sequence 35, Appl1
27	23	74.2	7	21	US-09-753-078-19	Sequence 19, Appl1
28	23	74.2	7	23	US-09-972-772-6	Sequence 6, Appl1
29	23	74.2	7	23	US-09-972-772-35	Sequence 35, Appl1
30	22	71.0	7	21	US-09-704-251-7	Sequence 7, Appl1
31	22	71.0	7	21	US-09-704-251-8	Sequence 8, Appl1
32	22	71.0	7	23	US-09-972-772-7	Sequence 7, Appl1
33	22	71.0	7	23	US-09-972-772-8	Sequence 8, Appl1
34	21	67.7	4	15	US-09-101-167-23	Sequence 23, Appl1
35	21	67.7	4	15	US-09-168-010-15	Sequence 15, Appl1
36	21	67.7	4	15	US-09-168-010-20	Sequence 20, Appl1
37	21	67.7	4	15	US-09-168-010-21	Sequence 21, Appl1
38	21	67.7	4	17	US-09-343-650-15	Sequence 15, Appl1
39	21	67.7	4	17	US-09-343-650-20	Sequence 20, Appl1
40	21	67.7	4	17	US-09-343-650-21	Sequence 21, Appl1
41	21	67.7	4	21	US-09-704-251-13	Sequence 13, Appl1
42	21	67.7	4	22	US-09-808-832-203	Sequence 203, Appl1
43	21	67.7	4	23	US-09-972-772-13	Sequence 13, Appl1
44	21	67.7	5	22	US-09-808-832-8	Sequence 8, Appl1
45	21	67.7	5	22	US-09-808-832-16	Sequence 16, Appl1

## ALIGNMENTS

RESULT 1  
US-09-753-078-18  
Sequence 18, Application US/09753078  
GENERAL INFORMATION:  
APPLICANT: Quirk, Stephen  
TITLE OF INVENTION: Use of Matrix Metalloproteinase Peptide Substrates to Lower  
FILE REFERENCE: 11301-0210/44039-227523  
CURRENT FILING DATE: 2000-12-29  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 18  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Synthetic Peptide  
US-09-753-078-18

Query Match 96.8%; Score 30; DB 21; Length 7;  
Best Local Similarity 85.7%; Pred. No. 2.9e+06;  
Matches 6; Conservative 0; Mismatches 1; Indels 0;

OY 1 p1g1xar 7  
||| |  
Db 1 PLGLAAR 7

RESULT 2  
US-09-168-010-14  
Sequence 14, Application US/09168010

```

: GENERAL INFORMATION:
: APPLICANT: The Liposome Company Inc.
: APPLICANT: Pak, Charles
: APPLICANT: Meers, Paul
: APPLICANT: Ali, Shaikat
: APPLICANT: Janoff, Andrew S.
: APPLICANT: Franklin, J. Craig
: APPLICANT: Erukulla, Ravi K.
: APPLICANT: Cabral-Lilly, Donna
: TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
: TITLE OF INVENTION: Delivery Using Same
: FILE REFERENCE: TLC 215B
: CURRENT APPLICATION NUMBER: US/09/168,010
: CURRENT FILING DATE: 1998-10-08
: EARLIER APPLICATION NUMBER: US 60/027,544
: EARLIER FILING DATE: 1996-10-15
: NUMBER OF SEQ ID NOS: 44
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 14
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Peptides
: FEATURE:
: NAME/KEY: VARIANT
: LOCATION: (5)...(5)
: OTHER INFORMATION: N-3-(2,4-dinitrophenyl)-L-2,3-diaminopropionyl
: FEATURE:
: NAME/KEY: BINDING
: LOCATION: (7)...(7)
: OTHER INFORMATION: C-terminal amino group
US-09-168-010-14
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```

Query Match          93.5%; Score 29; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 p1g1xar 7
    |||||
Db 1 PLGLXAR 7
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```

RESULT 3
US-09-248-158-1
: Sequence 1, Application US/09248158
: GENERAL INFORMATION:
: APPLICANT: Yuan, Zhengyu
: APPLICANT: Chen, Zhong-Xiao
: TITLE OF INVENTION: Direct Adsorption Scintillation Assay
: TITLE OF INVENTION: for Measuring Enzyme Activity and Assaying Biochemical
: TITLE OF INVENTION: Processes
: FILE REFERENCE: 342312000600
: CURRENT APPLICATION NUMBER: US/09/248,158
: CURRENT FILING DATE: 1999-02-09
: PRIOR APPLICATION NUMBER: 60/074,272
: PRIOR FILING DATE: 1998-02-10
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Unknown
: FEATURE:
: OTHER INFORMATION: Synthetic peptide
: NAME/KEY: MOD_RES
: LOCATION: (2)...(2)
: OTHER INFORMATION: 3H attached to leucine
US-09-248-158-1
```

```

Query-Match          93.5%; Score 29; DB 16; Length 7;
Best Local Similarity 85.7%; Pred. No. 2.9e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

Qy 1 p1g1xar 7
    |||||
Db 1 PLGLXAR 7
```

```

RESULT 4
US-09-343-650-14
: Sequence 14, Application US/09343650
: GENERAL INFORMATION:
: APPLICANT: The Liposome Company Inc.
: APPLICANT: Meers, Paul
: APPLICANT: Pak, Charles
: APPLICANT: Ali, Shaikat
: APPLICANT: Janoff, Andrew S.
: APPLICANT: Franklin, J. Craig
: APPLICANT: Erukulla, Ravi K.
: APPLICANT: Cabral-Lilly, Donna
: TITLE OF INVENTION: Peptide-Lipid Conjugates, Liposomes and
: TITLE OF INVENTION: Liposomal Drug Delivery
: FILE REFERENCE: TLC 215c
: CURRENT APPLICATION NUMBER: US/09/343,650
: CURRENT FILING DATE: 1999-06-29
: EARLIER APPLICATION NUMBER: US 08/950,618
: EARLIER FILING DATE: 1997-10-15
: NUMBER OF SEQ ID NOS: 44
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 14
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Peptides
: FEATURE:
: NAME/KEY: VARIANT
: LOCATION: (5)...(5)
: OTHER INFORMATION: N-3-(2,4-dinitrophenyl)-L-2,3-diaminopropionyl
: FEATURE:
: NAME/KEY: BINDING
: LOCATION: (7)...(7)
: OTHER INFORMATION: C-terminal amino group
US-09-343-650-14
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```

Query Match          93.5%; Score 29; DB 17; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 1 p1g1xar 7
    |||||
Db 1 PLGLXAR 7
```

```

RESULT 5
US-09-464-908A-1
: Sequence 1, Application US/09464908A
: GENERAL INFORMATION:
: APPLICANT: Aventis Pharmaceuticals, Inc.
: APPLICANT: Marshawsky, Alan
: APPLICANT: Janusz, Michael
: TITLE OF INVENTION: Selective Inhibitors of MMP-12
: FILE REFERENCE: HMR2026A US
: CURRENT APPLICATION NUMBER: US/09/464,908A
: CURRENT FILING DATE: 1999-12-17
: PRIOR APPLICATION NUMBER: 60/155,223
: PRIOR FILING DATE: 1998-12-31
: NUMBER OF SEQ ID NOS: 1
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 1
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: Synthetic Construct
: NAME/KEY: MISC_FEATURE
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LOCATION: (5)..(5)  
OTHER INFORMATION: Xaa at position 5 is N-3-(2,4-dinitrophenyl)-L-2,3-diaminopropion  
OTHER INFORMATION: y1  
US-09-464-908A-1

Query Match 93.5%; Score 29; DB 18; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.9e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglxar 7  
|||||  
Db 1 PLGLXAR 7

RESULT 6  
US-09-753-078-8  
Sequence 8, Application US/09753078  
GENERAL INFORMATION:  
APPLICANT: Quirk, Stephen  
APPLICANT: McGrath, Kevin  
TITLE OF INVENTION: Use of Matrix Metalloproteinase Peptide Substrates to Lower the  
FILE REFERENCE: 11301-0210/44039-227523  
CURRENT APPLICATION NUMBER: US/09/753,078  
CURRENT FILING DATE: 2000-12-29  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 8  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Synthetic Peptide  
US-09-753-078-8

Query Match 93.5%; Score 29; DB 21; Length 7;  
Best Local Similarity 85.7%; Pred. No. 2.9e+06;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglxar 7  
|||||  
Db 1 PLGLXAR 7

RESULT 7  
US-09-808-832-209  
Sequence 209, Application US/09808832  
GENERAL INFORMATION:  
APPLICANT: DuPont Pharmaceuticals Company  
TITLE OF INVENTION: Peptidase-cleavable, targeted antineoplastic drugs and their ther  
TITLE OF INVENTION: use  
FILE REFERENCE: PH-7134  
CURRENT APPLICATION NUMBER: US/09/808,832  
CURRENT FILING DATE: 2001-03-15  
PRIOR APPLICATION NUMBER: 60/189,387  
PRIORITY FILING DATE: 2000-03-15  
NUMBER OF SEQ ID NOS: 210  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 209  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (5)..(5)  
OTHER INFORMATION: diphenylalanine  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(7)  
OTHER INFORMATION: The synthesis of this peptide may be performed on an ABI 433A per  
OTHER INFORMATION: tide synthesizer using readily available materials well known to  
US-09-808-832-209

Query Match 93.5%; Score 29; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.9e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plglxar 7  
|||||  
Db 1 PLGLXAR 7

RESULT 8  
US-09-753-078-7  
Sequence 7, Application US/09753078  
GENERAL INFORMATION:  
APPLICANT: Quirk, Stephen  
APPLICANT: McGrath, Kevin  
TITLE OF INVENTION: Use of Matrix Metalloproteinase Peptide Substrates to Lower  
FILE REFERENCE: 11301-0210/44039-227523  
CURRENT APPLICATION NUMBER: US/09/753,078  
CURRENT FILING DATE: 2000-12-29  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 7  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Synthetic Peptide  
US-09-753-078-7

Query Match 90.3%; Score 28; DB 21; Length 7;  
Best Local Similarity 85.7%; Pred. No. 2.9e+06;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglxar 7  
|||||  
Db 1 PLGLXAR 7

RESULT 9  
US-09-753-078-16  
Sequence 16, Application US/09753078  
GENERAL INFORMATION:  
APPLICANT: Quirk, Stephen  
APPLICANT: McGrath, Kevin  
TITLE OF INVENTION: Use of Matrix Metalloproteinase Peptide Substrates to Lower  
FILE REFERENCE: 11301-0210/44039-227523  
CURRENT APPLICATION NUMBER: US/09/753,078  
CURRENT FILING DATE: 2000-12-29  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 16  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Synthetic Peptide  
US-09-753-078-16

Query Match 90.3%; Score 28; DB 21; Length 7;  
Best Local Similarity 85.7%; Pred. No. 2.9e+06;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglxar 7  
|||||  
Db 1 PLGLXAR 7

RESULT 10  
US-09-753-078-6  
Sequence 6, Application US/09753078  
GENERAL INFORMATION:  
APPLICANT: Quirk, Stephen

APPLICANT: McGrath, Kevin  
TITLE OF INVENTION: Use of Matrix Metalloproteinase Peptide Substrates to Lower the  
FILE REFERENCE: 11301-0210/44039-227523  
CURRENT APPLICATION NUMBER: US/09/753,078  
CURRENT FILING DATE: 2000-12-29  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patentin version 3.0  
SEQ ID NO 6  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Synthetic Peptide  
US-09-753-078-6

Query Match 77.4%; Score 24; DB 21; Length 7;  
Best Local Similarity 71.4%; Pred. No. 2.9e+06;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 plglxa 7  
11111  
DB 1 PLGLXAR 7

RESULT 11  
US-08-909-601-34

Sequence 34, Application US/08909601B  
GENERAL INFORMATION:  
APPLICANT: Russell, Stephen J  
APPLICANT: Cosset, Francois-Loic  
APPLICANT: Morling, Frances J  
APPLICANT: Nilson, Bo Harald Kurt  
APPLICANT: Peng, Kah-why  
TITLE OF INVENTION: Recombinant Viruses Incorporating a Protease Cleavable  
FILE REFERENCE: Atty Docket No: 03789/08913  
CURRENT APPLICATION NUMBER: US/08/909,601B  
CURRENT FILING DATE: 1997-08-12  
EARLIER APPLICATION NUMBER: GB9519691.1  
EARLIER FILING DATE: 1995-09-27  
EARLIER APPLICATION NUMBER: GB9523225.2  
EARLIER FILING DATE: 1995-11-14  
EARLIER APPLICATION NUMBER: GB9604562.0  
EARLIER FILING DATE: 1996-03-04  
EARLIER APPLICATION NUMBER: PCT/GB/02381  
EARLIER FILING DATE: 1999-09-27  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 34  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: GLA and  
OTHER INFORMATION: M71-MMP protease cleavage site peptide sequence.  
US-08-909-601-34

Query Match 74.2%; Score 23; DB 13; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.9e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglxa 6  
11111  
DB 1 PLGLMA 6

RESULT 12  
US-08-909-601-34  
Sequence 34, Application US/08909601C  
GENERAL INFORMATION:  
APPLICANT: Russell, Stephen J  
APPLICANT: Cosset, Francois-Loic

APPLICANT: Morling, Frances J  
APPLICANT: Nilson, Bo Harald Kurt  
APPLICANT: Peng, Kah-why  
TITLE OF INVENTION: Recombinant Viruses Incorporating a Protease Cleavable  
FILE REFERENCE: Atty Docket No: 03789/08913  
CURRENT APPLICATION NUMBER: US/08/909,601C  
CURRENT FILING DATE: 1997-08-12  
PRIOR APPLICATION NUMBER: GB9519691.1  
PRIOR FILING DATE: 1995-09-27  
PRIOR APPLICATION NUMBER: GB9523225.2  
PRIOR FILING DATE: 1995-11-14  
PRIOR APPLICATION NUMBER: GB9604562.0  
PRIOR FILING DATE: 1996-03-04  
PRIOR APPLICATION NUMBER: PCT/GB/02381  
PRIOR FILING DATE: 1999-09-27  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 34  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: GLA and  
OTHER INFORMATION: M71-MMP protease cleavage site peptide sequence.  
US-08-909-601-34

Query Match 74.2%; Score 23; DB 13; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.9e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglxa 6  
11111  
DB 1 PLGLMA 6

RESULT 13  
US-08-909-607-34

Sequence 34, Application US/08909607A  
GENERAL INFORMATION:  
APPLICANT: Russell, Stephen J  
APPLICANT: Cosset, Francois-Loic  
APPLICANT: Morling, Frances J  
APPLICANT: Nilson, Bo Harald Kurt  
APPLICANT: Peng, Kah-why  
TITLE OF INVENTION: Recombinant Viruses Incorporating a Protease Cleavable  
FILE REFERENCE: Atty Docket No: 03789/08913  
CURRENT APPLICATION NUMBER: US/08/909,607A  
CURRENT FILING DATE: 1997-08-12  
EARLIER APPLICATION NUMBER: GB9519691.1  
EARLIER FILING DATE: 1995-09-27  
EARLIER APPLICATION NUMBER: GB9523225.2  
EARLIER FILING DATE: 1995-11-14  
EARLIER APPLICATION NUMBER: GB9604562.0  
EARLIER FILING DATE: 1996-03-04  
EARLIER APPLICATION NUMBER: PCT/GB/02381  
EARLIER FILING DATE: 1999-09-27  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 34  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: GLA and  
OTHER INFORMATION: M71-MMP protease cleavage site peptide sequence.  
US-08-909-607-34

Query Match 74.2%; Score 23; DB 13; Length 6;  
Best Local Similarity 83.3%; Pred. No. 2.9e+06;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 plg1xa 6  
 11111  
 Db 1 PLGLMA 6

Db 1 PLGLMA 6

Search completed: March 1, 2002, 06:55:11  
 Job time: 183 sec

RESULT 14  
 US-09-496-231A-30  
 ; Sequence 30, Application US/09496231A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hubbell, Jeffrey A.  
 ; APPLICANT: Elbert, Donald  
 ; APPLICANT: Lutolf, Mathias  
 ; APPLICANT: Priat, Alison  
 ; APPLICANT: Schoenmakers, Ronald  
 ; APPLICANT: Tirelli, Nicola  
 ; APPLICANT: Vernon, Brent  
 ; TITLE OF INVENTION: BIOMATERIALS FORMED BY NUCLEOPHILIC  
 ; TITLE OF INVENTION: ADDITION REACTION TO CONJUGATED UNSATURATED GROUPS  
 ; FILE REFERENCE: 50154/002002  
 ; CURRENT APPLICATION NUMBER: US/09/496,231A  
 ; CURRENT FILING DATE: 2000-02-01  
 ; PRIOR APPLICATION NUMBER: 60/118,093  
 ; PRIOR FILING DATE: 1999-02-01  
 ; NUMBER OF SEQ ID NOS: 74  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 30  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-496-231A-30

Query Match 74.2%; Score 23; DB 18; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2.9e+06;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 plg1xa 6  
 11111  
 Db 1 PLGLMA 6

RESULT 15  
 US-09-561-005-24  
 ; Sequence 24, Application US/09561005  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Philip E. Thorpe  
 ; APPLICANT: Rolf A. Brekken  
 ; TITLE OF INVENTION: ANTIBODY CONJUGATE METHODS FOR SELECTIVELY INHIBITING VEGF  
 ; FILE REFERENCE: 4001,002585  
 ; CURRENT APPLICATION NUMBER: US/09/561,005  
 ; CURRENT FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: 60/131,432  
 ; PRIOR FILING DATE: 1999-04-28  
 ; NUMBER OF SEQ ID NOS: 44  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 24  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
 ; OTHER INFORMATION: PEPTIDE  
 US-09-561-005-24

Query Match 74.2%; Score 23; DB 19; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2.9e+06;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 plg1xa 6  
 11111



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OM protein - protein search, using sw model

Run on: March 1, 2002, 06:51:53 ; Search time 13.1 Seconds  
(without alignments)  
24.004 Million cell updates/sec

Title: 09-876091-2  
Perfect score: 31  
Sequence: 1 plglxar 7

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 216105 seqs, 44922408 residues

Total number of hits satisfying chosen parameters: 13266

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_New:\*  
1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/ptodata/1/paa/US610\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74.2	6	5	US-09-560-390-25	Sequence 25, Appl
2	74.2	6	5	US-09-998-831-24	Sequence 24, Appl
3	74.2	7	5	US-09-560-390-29	Sequence 29, Appl
4	74.2	7	6	US-10-001-945-6	Sequence 6, Appl
5	74.2	7	6	US-10-001-945-35	Sequence 35, Appl
6	71.0	7	5	US-09-560-390-26	Sequence 26, Appl
7	71.0	7	6	US-10-001-945-7	Sequence 7, Appl
8	71.0	7	6	US-10-001-945-8	Sequence 8, Appl
9	67.7	4	6	US-10-001-945-13	Sequence 13, Appl
10	67.7	5	5	US-09-560-390-32	Sequence 32, Appl
11	67.7	6	5	US-09-560-390-22	Sequence 22, Appl
12	61.3	7	1	PCT-US01-28124A-22	Sequence 22, Appl
13	61.3	7	1	PCT-US01-27692A-22	Sequence 22, Appl
14	61.3	7	5	US-09-394-019A-221	Sequence 22, Appl
15	61.3	7	6	US-10-001-945-5	Sequence 5, Appl
16	54.8	4	5	US-09-451-206-17	Sequence 17, Appl
17	54.8	4	5	US-09-914-541-22	Sequence 22, Appl
18	54.8	4	6	US-10-001-945-1	Sequence 1, Appl
19	54.8	4	6	US-10-001-945-14	Sequence 14, Appl
20	54.8	4	6	US-10-001-945-27	Sequence 27, Appl
21	54.8	5	1	PCT-US01-27692A-71	Sequence 71, Appl
22	54.8	5	1	PCT-US01-27702A-256	Sequence 256, App
23	54.8	5	5	US-09-560-390-2	Sequence 2, Appl
24	54.8	5	5	US-09-560-390-18	Sequence 18, Appl
25	54.8	5	5	US-09-560-390-21	Sequence 21, Appl
26	54.8	5	5	US-09-560-390-24	Sequence 24, Appl

27	17	54.8	5	5	US-09-104-337A-321	Sequence 321, App
28	17	54.8	6	5	US-09-560-390-5	Sequence 5, Appl
29	17	54.8	7	1	PCT-US01-28044A-301	Sequence 301, App
30	17	54.8	7	5	US-09-560-390-27	Sequence 27, Appl
31	17	54.8	7	5	US-09-560-390-33	Sequence 33, Appl
32	17	54.8	7	5	US-09-873-676-92	Sequence 92, Appl
33	17	54.8	7	6	US-10-001-945-9	Sequence 9, Appl
34	16	51.6	7	5	US-09-029-047C-13	Sequence 13, Appl
35	16	51.6	7	5	US-09-935-291A-16	Sequence 16, Appl
36	15	48.4	5	5	US-09-560-390-19	Sequence 19, Appl
37	15	48.4	6	1	PCT-US01-27702A-268	Sequence 268, App
38	15	48.4	6	6	US-10-001-945-19	Sequence 19, Appl
39	15	48.4	7	1	PCT-US01-27692A-83	Sequence 83, Appl
40	15	48.4	7	1	PCT-US01-28044A-198	Sequence 198, Appl
41	15	48.4	7	5	US-09-758-128-48	Sequence 48, Appl
42	15	48.4	7	5	US-09-758-426-48	Sequence 48, Appl
43	15	48.4	7	5	US-09-758-138-48	Sequence 48, Appl
44	15	48.4	7	5	US-09-500-904A-63	Sequence 63, Appl
45	14	45.2	4	5	US-09-620-394B-8933	Sequence 8933, Ap

## ALIGNMENTS

RESULT 1  
US-09-560-390-25  
: Sequence 25, Application US/09560390  
: GENERAL INFORMATION:  
: APPLICANT: Pachence Ph.D., James M.  
: APPLICANT: Belinka, Benjamin A.  
: TITLE OF INVENTION: ENZYMATICALLY ACTIVATED POLYMERIC DRUG CONJUGATES  
: FILE REFERENCE: 114914.102  
: CURRENT APPLICATION NUMBER: US/09/560.390  
: NUMBER OF SEQ ID NOS: 35  
: SOFTWARE: PatentIn Ver. 2.1  
: SEQ ID NO 25  
: LENGTH: 6  
: TYPE: PRT  
: ORGANISM: Homo sapiens  
US-09-560-390-25

Query Match 74.2% Score 23; DB 5; Length 6;  
Best local Similarity 83.3% Pred. No. 1.9e+05; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 1;

Oy 1 plglxa 6  
|||||  
Db 1 PLGLWA 6

RESULT 2  
US-09-998-831-24  
: Sequence 24, Application US/09998831  
: GENERAL INFORMATION:  
: APPLICANT: Philip E. Thorpe  
: APPLICANT: Rolf A. Brecken  
: TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY  
: FILE REFERENCE: 4001.002584  
: CURRENT APPLICATION NUMBER: US/09/998.831  
: CURRENT FILING DATE: 2001-11-30  
: PRIOR APPLICATION NUMBER: 09/561,108  
: PRIOR FILING DATE: 2000-04-28  
: NUMBER OF SEQ ID NOS: 44  
: SOFTWARE: PatentIn Ver. 2.0  
: SEQ ID NO 24  
: LENGTH: 6  
: TYPE: PRT  
: ORGANISM: Artificial Sequence  
: FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
OTHER INFORMATION: PEPTIDE  
US-09-998-831-24

Query Match 74.2%; Score 23; DB 5; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1.9e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglxa 6  
|||||  
DB 1 PLGLWA 6

RESULT 3  
US-09-560-390-29  
Sequence 29, Application US/09560390

GENERAL INFORMATION:  
APPLICANT: Pachence Ph.D., James M.  
APPLICANT: Belinka, Benjamin A.  
APPLICANT: Ramani, Tnulas  
TITLE OF INVENTION: ENZYMATICALLY ACTIVATED POLYMERIC DRUG CONJUGATES  
FILE REFERENCE: 114914.102  
CURRENT APPLICATION NUMBER: US/09/560.390  
CURRENT FILING DATE: 2000-04-28  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 29  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-560-390-29

Query Match 74.2%; Score 23; DB 5; Length 7;  
Best Local Similarity 57.1%; Pred. No. 1.9e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglxar 7  
|||||:  
DB 1 PLGMSMR 7

RESULT 4  
US-10-001-945-6  
Sequence 6, Application US/10001945

GENERAL INFORMATION:  
APPLICANT: Olson, Gary L.  
APPLICANT: Self, Christopher  
APPLICANT: Lee, Lilly  
APPLICANT: Cook, Charles M.  
APPLICANT: Birktoft, Jens  
TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE  
FILE REFERENCE: PPI-106CP2  
CURRENT APPLICATION NUMBER: US/10/001.945  
CURRENT FILING DATE: 2001-11-01  
PRIOR APPLICATION NUMBER: US 09/972.772  
PRIOR FILING DATE: 2001-10-05  
PRIOR APPLICATION NUMBER: US 09/704.251  
PRIOR FILING DATE: 2000-11-01  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Motifs  
NAME/KEY: VARIANT  
LOCATION: 7  
OTHER INFORMATION: Xaa at position 7 represents D-Arginine  
US-10-001-945-6

Query Match 74.2%; Score 23; DB 6; Length 7;  
Best Local Similarity 83.3%; Pred. No. 1.9e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglxa 6  
|||||  
DB 1 PLGLWA 6

RESULT 5  
US-10-001-945-35  
Sequence 35, Application US/10001945

GENERAL INFORMATION:  
APPLICANT: Olson, Gary L.  
APPLICANT: Self, Christopher  
APPLICANT: Lee, Lilly  
APPLICANT: Cook, Charles M.  
APPLICANT: Birktoft, Jens  
TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE  
FILE REFERENCE: PPI-106CP2  
CURRENT APPLICATION NUMBER: US/10/001.945  
CURRENT FILING DATE: 2001-11-01  
PRIOR APPLICATION NUMBER: US 09/972.772  
PRIOR FILING DATE: 2001-10-05  
PRIOR APPLICATION NUMBER: US 09/704.251  
PRIOR FILING DATE: 2000-11-01  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 35  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Motifs  
US-10-001-945-35

Query Match 74.2%; Score 23; DB 6; Length 7;  
Best Local Similarity 57.1%; Pred. No. 1.9e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglxar 7  
|||||:  
DB 1 PLGMSMR 7

RESULT 6

US-09-560-390-26  
Sequence 26, Application US/09560390  
GENERAL INFORMATION:  
APPLICANT: Pachence Ph.D., James M.  
APPLICANT: Belinka, Benjamin A.  
APPLICANT: Ramani, Tnulas  
TITLE OF INVENTION: ENZYMATICALLY ACTIVATED POLYMERIC DRUG CONJUGATES  
FILE REFERENCE: 114914.102  
CURRENT APPLICATION NUMBER: US/09/560.390  
CURRENT FILING DATE: 2000-04-28  
NUMBER OF SEQ ID NOS: 35  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 26  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-560-390-26

Query Match 71.0%; Score 22; DB 5; Length 7;  
Best Local Similarity 71.4%; Pred. No. 1.9e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 plglxar 7  
|||  
Db 1 PLALMAR 7

RESULT 7  
US-10-001-945-7  
; Sequence 7, Application US/10001945  
; GENERAL INFORMATION:  
; APPLICANT: Olson, Gary L.  
; APPLICANT: Self, Christopher  
; APPLICANT: Lee, Lily  
; APPLICANT: Cook, Charles M.  
; APPLICANT: Birktoft, Jens  
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE  
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS  
; FILE REFERENCE: PPI-106CP2  
; CURRENT APPLICATION NUMBER: US/10/001,945  
; CURRENT FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 09/972,772  
; PRIOR FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: US 09/704,251  
; PRIOR FILING DATE: 2000-11-01  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Motifs  
US-10-001-945-7

Query Match 71.0%; Score 22; DB 6; Length 7;  
Best Local Similarity 71.4%; Pred. No. 1.9e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 plglxar 7  
|||  
Db 1 PLALMAR 7

RESULT 8  
US-10-001-945-8  
; Sequence 8, Application US/10001945  
; GENERAL INFORMATION:  
; APPLICANT: Olson, Gary L.  
; APPLICANT: Self, Christopher  
; APPLICANT: Lee, Lily  
; APPLICANT: Cook, Charles M.  
; APPLICANT: Birktoft, Jens  
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE  
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS  
; FILE REFERENCE: PPI-106CP2  
; CURRENT APPLICATION NUMBER: US/10/001,945  
; CURRENT FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 09/972,772  
; PRIOR FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: US 09/704,251  
; PRIOR FILING DATE: 2000-11-01  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Motifs  
US-10-001-945-8

Query Match 71.0%; Score 22; DB 6; Length 7;

Best Local Similarity 71.4%; Pred. No. 1.9e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 plglxar 7  
|||  
Db 1 PLALMAR 7

RESULT 9  
US-10-001-945-13  
; Sequence 13, Application US/10001945  
; GENERAL INFORMATION:  
; APPLICANT: Olson, Gary L.  
; APPLICANT: Self, Christopher  
; APPLICANT: Lee, Lily  
; APPLICANT: Cook, Charles M.  
; APPLICANT: Birktoft, Jens  
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE  
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS  
; FILE REFERENCE: PPI-106CP2  
; CURRENT APPLICATION NUMBER: US/10/001,945  
; CURRENT FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 09/972,772  
; PRIOR FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: US 09/704,251  
; PRIOR FILING DATE: 2000-11-01  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Motifs  
US-10-001-945-13

Query Match 67.7%; Score 21; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 plgl 4  
|||  
Db 1 PLGL 4

RESULT 10  
US-09-560-390-32  
; Sequence 32, Application US/09560390  
; GENERAL INFORMATION:  
; APPLICANT: Pachence Ph.D., James M.  
; APPLICANT: Bellinka, Benjamin A.  
; APPLICANT: Ramani, Thulasi  
; TITLE OF INVENTION: ENZYMATICALLY ACTIVATED POLYMERIC DRUG CONJUGATES  
; FILE REFERENCE: 114914.102  
; CURRENT APPLICATION NUMBER: US/09/560,390  
; CURRENT FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-560-390-32

Query Match 67.7%; Score 21; DB 5; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.9e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 plgl 4  
|||  
Db 1 PLGL 4

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RESULT 11
US-09-560-390-22
; Sequence 22, Application US/09560390
; GENERAL INFORMATION:
; APPLICANT: Pachence Ph.D., James M.
; APPLICANT: Belinka, Benjamin A.
; APPLICANT: Ramani, Thulasi
; TITLE OF INVENTION: ENZYMATICALLY ACTIVATED POLYMERIC DRUG CONJUGATES
; FILE REFERENCE: 114914.102
; CURRENT APPLICATION NUMBER: US/09/560,390
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-560-390-22

Query Match          67.7%; Score 21; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
   |||
Db 1 PLGL 4

RESULT 12
PCT-US01-28124A-22
; Sequence 22, Application PC/TUS0128124A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Biopanning and Rapid Analysis of Selective Interactive Ligands (H
; FILE REFERENCE: 005774.P004PCP
; CURRENT APPLICATION NUMBER: PCT/US01/28124A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(6)
; OTHER INFORMATION: synthetic construct
PCT-US01-28124A-22

Query Match          61.3%; Score 19; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 glxar 7
   |||
Db 1 GLSAR 5

RESULT 13
PCT-US01-27692A-42
; Sequence 42, Application PC/TUS0127692A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCP
; CURRENT APPLICATION NUMBER: PCT/US01/27692A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
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```
; SEQ ID NO 42
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(7)
; OTHER INFORMATION: synthetic construct
PCT-US01-27692A-42

Query Match          61.3%; Score 19; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 lgxar 7
   |||
Db 1 VGLHAR 6

RESULT 14
US-09-394-019A-221
; Sequence 221, Application US/09394019A
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICA
; FILE REFERENCE: 300-903820US
; CURRENT APPLICATION NUMBER: US/09/394,019A
; CURRENT FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: US 08/802,981
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 221
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide substrate
; NAME/KEY: Artificial
; LOCATION: (1)..(5)
; OTHER INFORMATION: Artificial protease substrate
US-09-394-019A-221

Query Match          61.3%; Score 19; DB 5; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 plgl 4
   |||
Db 1 PLGI 4

RESULT 15
US-10-001-945-5
; Sequence 5, Application US/10001945
; GENERAL INFORMATION:
; APPLICANT: Olson, Gary L.
; APPLICANT: Self, Christopher
; APPLICANT: Lee, Lily
; APPLICANT: Cook, Charles M.
; APPLICANT: Birktoft, Jens
; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR THE
; TITLE OF INVENTION: MODULATION OF ANGIOGENESIS
; FILE REFERENCE: PPT-106CP2
; CURRENT APPLICATION NUMBER: US/10/001,945
; CURRENT FILING DATE: 2001-11-01
```



```

; PRIOR APPLICATION NUMBER: US 09/972,772
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 09/704,251
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Motifs
; NAME/KEY: VARIANT
; LOCATION: 4
; OTHER INFORMATION: Xaa at position 4 represents methylated cysteine
; NAME/KEY: VARIANT
; LOCATION: 7
; OTHER INFORMATION: Xaa at position 7 represents D-Arginine
; US-10-001-945-5

```

```

Query Match          61.3%  Score 19; DB 6; Length 7;
Best Local Similarity 66.7%  Pred. NO. 1.9e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 p1g1xa 6
   111 1
Db 1 PLGXHA 6

```

Search completed: March 1, 2002, 06:53:34  
 Job time: 101 sec

2

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2002, 06:50:43 ; Search time 12.58 Seconds  
(without alignments)  
12.522 Million cell updates/sec

Title: 09-876091-2  
Perfect score: 31  
Sequence: 1 plg1xar 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 35098

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfilest.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	93.5	7	1 US-08-303-270-7	Sequence 7, Appli
2	29	93.5	7	3 US-08-950-618-14	Sequence 14, Appli
3	29	93.5	7	4 US-09-168-010-14	Sequence 14, Appli
4	29	93.5	7	4 US-09-144-419A-3	Sequence 3, Appli
5	23	74.2	6	4 US-09-208-684-12	Sequence 12, Appli
6	21	67.7	4	3 US-08-950-618-15	Sequence 15, Appli
7	21	67.7	4	3 US-08-950-618-20	Sequence 20, Appli
8	21	67.7	4	3 US-08-950-618-21	Sequence 21, Appli
9	21	67.7	4	3 US-09-101-167-23	Sequence 23, Appli
10	21	67.7	4	4 US-09-168-010-15	Sequence 15, Appli
11	21	67.7	4	4 US-09-168-010-20	Sequence 20, Appli
12	21	67.7	4	4 US-09-168-010-21	Sequence 21, Appli
13	21	67.7	6	1 US-08-303-270-8	Sequence 8, Appli
14	21	67.7	6	4 US-08-281-313-8	Sequence 18, Appli
15	20	64.5	7	3 US-09-101-167-18	Sequence 18, Appli
16	20	64.5	7	3 US-09-101-167-21	Sequence 21, Appli
17	20	64.5	7	3 US-09-101-167-27	Sequence 27, Appli
18	19	61.3	7	4 US-09-258-754-11	Sequence 11, Appli
19	19	61.3	7	4 US-09-042-107-11	Sequence 11, Appli
20	18	58.1	5	4 US-08-793-701-9	Sequence 9, Appli
21	17	54.8	4	1 US-08-219-156-5	Sequence 5, Appli
22	17	54.8	4	1 US-08-238-089-5	Sequence 5, Appli
23	17	54.8	4	1 US-08-238-089-6	Sequence 6, Appli
24	17	54.8	4	1 US-08-366-783-8	Sequence 8, Appli
25	17	54.8	4	1 US-08-432-651A-5	Sequence 5, Appli
26	17	54.8	4	1 US-08-432-651A-6	Sequence 6, Appli
27	17	54.8	4	2 US-08-707-237A-97	Sequence 97, Appli

28	17	54.8	4	2 US-08-846-021A-11	Sequence 11, Appli
29	17	54.8	4	3 US-08-642-246-17	Sequence 17, Appli
30	17	54.8	4	3 US-08-962-962C-5	Sequence 5, Appli
31	17	54.8	4	3 US-08-962-962C-6	Sequence 6, Appli
32	17	54.8	4	5 PCT-US95-05560-5	Sequence 5, Appli
33	17	54.8	4	5 PCT-US95-05560-6	Sequence 6, Appli
34	17	54.8	4	5 PCT-US96-06229-17	Sequence 17, Appli
35	17	54.8	5	1 US-08-221-582A-4	Sequence 4, Appli
36	17	54.8	5	1 US-08-219-156-2	Sequence 2, Appli
37	17	54.8	5	1 US-08-219-156-4	Sequence 4, Appli
38	17	54.8	5	1 US-08-219-156-6	Sequence 6, Appli
39	17	54.8	5	1 US-08-219-156-7	Sequence 7, Appli
40	17	54.8	5	1 US-08-219-156-8	Sequence 8, Appli
41	17	54.8	5	1 US-08-238-089-31	Sequence 31, Appli
42	17	54.8	5	1 US-08-238-089-32	Sequence 32, Appli
43	17	54.8	5	1 US-08-213-897A-4	Sequence 4, Appli
44	17	54.8	5	1 US-08-213-897A-15	Sequence 15, Appli
45	17	54.8	5	1 US-08-432-651A-31	Sequence 31, Appli

## ALIGNMENTS

RESULT 1  
US-08-303-270-7  
Sequence 7, Application US/08303270  
Patent No. 5646027  
GENERAL INFORMATION:  
APPLICANT: Ye, Qi-Zhang  
APPLICANT: Johnson, Linda L.  
APPLICANT: Hupe, Donald J.  
TITLE OF INVENTION: Process for the Production of  
TITLE OF INVENTION: Gelatinase Catalytic Domain Protein  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Warner-Lambert Company  
STREET: 2800 Plymouth Rd.  
CITY: Ann Arbor  
STATE: MI  
COUNTRY: US  
ZIP: 48105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/303,270  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Timey, Francis J.  
REGISTRATION NUMBER: 33,069  
REFERENCE/DOCKET NUMBER: 5120-FJT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 313 996-7295  
TELEFAX: 313 996-1553  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-303-270-7

Query Match 93.5%; Score 29; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0;

Oy 1 plg1xar 7  
|||||||

```
DB      1  PLGLXAR 7

RESULT  2
US-08-950-618-14
; Sequence 14, Application US/08950618
; Patent No. 6087325
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; TITLE OF INVENTION: Methods of liposomal Drug Delivery using
; FILE REFERENCE: TLC 215A
; CURRENT APPLICATION NUMBER: US/08/950,618
; CURRENT FILING DATE: 1997-10-15
; EARLIER APPLICATION NUMBER: US 60/027,544
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Peptides
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (5)...(5)
; OTHER INFORMATION: N-3-(2,4-dinitrophenyl)-L-2,3-diaminopropionyl
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (7)...(7)
; OTHER INFORMATION: C-terminal amino group
US-08-950-618-14

Query Match      93.5%; Score 29; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  plglxar 7
        |||||
DB      1  PLGLXAR 7

RESULT  3
US-09-168-010-14
; Sequence 14, Application US/09168010A
; Patent No. 6143716
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; APPLICANT: Cabral-Lilly, Donna
; TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and
; FILE REFERENCE: TLC 215B
; CURRENT APPLICATION NUMBER: US/09/168,010A
; CURRENT FILING DATE: 1998-10-07
; EARLIER APPLICATION NUMBER: US 60/027,544
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT

; ORGANISM: Peptides
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (5)...(5)
; OTHER INFORMATION: N-3-(2,4-dinitrophenyl)-L-2,3-diaminopropionyl
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (7)...(7)
; OTHER INFORMATION: C-terminal amino group
US-09-168-010-14

Query Match      93.5%; Score 29; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  plglxar 7
        |||||
DB      1  PLGLXAR 7

RESULT  5
US-09-208-684-12
; Sequence 12, Application US/09208684
; Patent No. 6224903
; GENERAL INFORMATION:
; APPLICANT: Francis J. Martin
; APPLICANT: Samuel Zalipsky
; TITLE OF INVENTION: Polymer-Lipid Conjugate for Fusion of
; FILE REFERENCE: 5325-0148.32
; CURRENT APPLICATION NUMBER: US/09/208,684
; CURRENT FILING DATE: 1998-12-10
; EARLIER APPLICATION NUMBER: 08/949,046
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: 60/028,269
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
```

```
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-208-684-12
```

```
Query Match          74.2%; Score 23; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      1 plg1xa 6
        ||||| 1
Db       1 PLGLMA 6
```

```
RESULT      6
US-08-950-618-15
; Sequence 15, Application US/08950618
; Patent No. 6087325
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; TITLE OF INVENTION: Methods of Liposomal Drug Delivery Using
; TITLE OF INVENTION: Peptidase-Cleavable Fusogenic Phospholipids
; FILE REFERENCE: TIC 215A
; CURRENT APPLICATION NUMBER: US/08/950,618
; CURRENT FILING DATE: 1997-10-15
; EARLIER APPLICATION NUMBER: US 60/027,544
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
US-08-950-618-15
```

```
Query Match          67.7%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 plg1 4
        |||||
Db       1 PLGL 4
```

```
RESULT      7
US-08-950-618-20
; Sequence 20, Application US/08950618
; Patent No. 6087325
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; TITLE OF INVENTION: Methods of Liposomal Drug Delivery Using
; TITLE OF INVENTION: Peptidase-Cleavable Fusogenic Phospholipids
; FILE REFERENCE: TIC 215A
; CURRENT APPLICATION NUMBER: US/08/950,618
; CURRENT FILING DATE: 1997-10-15
; EARLIER APPLICATION NUMBER: US 60/027,544
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
```

```
; SEQ ID NO 20
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)...(1)
; OTHER INFORMATION: N-terminal methoxy succinyl group
US-08-950-618-20
```

```
Query Match          67.7%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 plg1 4
        |||||
Db       1 PLGL 4
```

```
RESULT      8
US-08-950-618-21
; Sequence 21, Application US/08950618
; Patent No. 6087325
; GENERAL INFORMATION:
; APPLICANT: The Liposome Company Inc.
; APPLICANT: Pak, Charles
; APPLICANT: Meers, Paul
; APPLICANT: Ali, Shaukat
; APPLICANT: Janoff, Andrew S.
; APPLICANT: Franklin, J. Craig
; APPLICANT: Erukulla, Ravi K.
; TITLE OF INVENTION: Methods of Liposomal Drug Delivery Using
; TITLE OF INVENTION: Peptidase-Cleavable Fusogenic Phospholipids
; FILE REFERENCE: TIC 215A
; CURRENT APPLICATION NUMBER: US/08/950,618
; CURRENT FILING DATE: 1997-10-15
; EARLIER APPLICATION NUMBER: US 60/027,544
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Peptides
; FEATURE:
; NAME/KEY: BINDING
; LOCATION: (1)...(1)
; OTHER INFORMATION: N-terminal succinyl group
US-08-950-618-21
```

```
Query Match          67.7%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 plg1 4
        |||||
Db       1 PLGL 4
```

```
RESULT      9
US-09-101-167-23
; Sequence 23, Application US/09101167B
; Patent No. 6127139
; GENERAL INFORMATION:
; APPLICANT: TE KOPELE, Johannes M
; APPLICANT: BEERMAN, Bob
; TITLE OF INVENTION: METHOD FOR ASSAYING PROTEOLYTIC ENZYMES USING
; TITLE OF INVENTION: FLUORESCENCE-QUENCHED SUBSTRATES
; FILE REFERENCE: TE KOPELE et al. 09/101,167
; CURRENT APPLICATION NUMBER: US/09/101,167B
; CURRENT FILING DATE: 1998-07-02
```

EARLIER APPLICATION NUMBER: EP 96200017.0  
EARLIER FILING DATE: 1996-01-04  
EARLIER APPLICATION NUMBER: PCT/NL97/00002  
EARLIER FILING DATE: 1997-01-02  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 23  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: UNKNOWN  
US-09-101-167-23

Query Match 67.7%; Score 21; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 plgl 4  
1111  
DB 1 PLGL 4

RESULT 10  
US-09-168-010-15  
Sequence 15, Application US/09168010A  
Patent No. 6143716  
GENERAL INFORMATION:  
APPLICANT: The Liposome Company Inc.  
APPLICANT: Pak, Charles  
APPLICANT: Meers, Paul  
APPLICANT: Ali, Shaikat  
APPLICANT: Janoff, Andrew S.  
APPLICANT: Franklin, J. Craig  
APPLICANT: Erukulla, Ravi K.  
APPLICANT: Cabral-Lilly, Donna  
TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and  
TITLE OF INVENTION: Delivery Using Same  
FILE REFERENCE: TLC 215B  
CURRENT APPLICATION NUMBER: US/09/168,010A  
CURRENT FILING DATE: 1998-10-07  
EARLIER APPLICATION NUMBER: US 60/027,544  
EARLIER FILING DATE: 1996-10-15  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 15  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Peptides  
US-09-168-010-15

Query Match 67.7%; Score 21; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 plgl 4  
1111  
DB 1 PLGL 4

RESULT 11  
US-09-168-010-20  
Sequence 20, Application US/09168010A  
Patent No. 6143716  
GENERAL INFORMATION:  
APPLICANT: The Liposome Company Inc.  
APPLICANT: Pak, Charles  
APPLICANT: Meers, Paul  
APPLICANT: Ali, Shaikat  
APPLICANT: Janoff, Andrew S.  
APPLICANT: Franklin, J. Craig

APPLICANT: Erukulla, Ravi K.  
APPLICANT: Cabral-Lilly, Donna  
TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and  
TITLE OF INVENTION: Delivery Using Same  
FILE REFERENCE: TLC 215B  
CURRENT APPLICATION NUMBER: US/09/168,010A  
CURRENT FILING DATE: 1998-10-07  
EARLIER APPLICATION NUMBER: US 60/027,544  
EARLIER FILING DATE: 1996-10-15  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 20  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Peptides  
FEATURE:  
NAME/KEY: BINDING  
LOCATION: (1)...(1)  
OTHER INFORMATION: N-terminal methoxy succinyl group  
US-09-168-010-20

Query Match 67.7%; Score 21; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 plgl 4  
1111  
DB 1 PLGL 4

RESULT 12  
US-09-168-010-21  
Sequence 21, Application US/09168010A  
Patent No. 6143716  
GENERAL INFORMATION:  
APPLICANT: The Liposome Company Inc.  
APPLICANT: Pak, Charles  
APPLICANT: Meers, Paul  
APPLICANT: Ali, Shaikat  
APPLICANT: Janoff, Andrew S.  
APPLICANT: Franklin, J. Craig  
APPLICANT: Erukulla, Ravi K.  
APPLICANT: Cabral-Lilly, Donna  
TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and  
TITLE OF INVENTION: Delivery Using Same  
FILE REFERENCE: TLC 215B  
CURRENT APPLICATION NUMBER: US/09/168,010A  
CURRENT FILING DATE: 1998-10-07  
EARLIER APPLICATION NUMBER: US 60/027,544  
EARLIER FILING DATE: 1996-10-15  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 21  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Peptides  
FEATURE:  
NAME/KEY: BINDING  
LOCATION: (1)...(1)  
OTHER INFORMATION: N-terminal succinyl group  
US-09-168-010-21

Query Match 67.7%; Score 21; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 plgl 4  
1111  
DB 1 PLGL 4

RESULT 13  
US-08-303-270-8  
Sequence 8, Application US/08303270  
Patent No. 5646027  
GENERAL INFORMATION:  
APPLICANT: Ye, Qi-Zhuang  
APPLICANT: Johnson, Linda L.  
APPLICANT: Hupe, Donald J.  
TITLE OF INVENTION: Process for the Production of  
TITLE OF INVENTION: Gelatinase Catalytic Domain Protein  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Warner-Lambert Company  
STREET: 2800 Plymouth Rd.  
CITY: Ann Arbor  
STATE: MI  
COUNTRY: US  
ZIP: 48105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/303,270  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Tinney, Francis J.  
REGISTRATION NUMBER: 33,069  
REFERENCE/DOCKET NUMBER: 5120-FJT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 313 996-7295  
TELEFAX: 313 996-1553  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Thiolester-bond  
LOCATION: 3..4  
US-08-303-270-8

Query Match 67.7%; Score 21; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 Plg1 4  
1111  
Db 1 PLGL 4

RESULT 14  
US-08-281-313-8  
Sequence 8, Application US/08281313  
Patent No. 6284513  
GENERAL INFORMATION:  
APPLICANT: Ye, Qi-Zhuang  
APPLICANT: Johnson, Linda L.  
APPLICANT: Hupe, Donald J.  
APPLICANT: Baragi, Vijaykumar  
TITLE OF INVENTION: Process for the Production of  
TITLE OF INVENTION: Stromelysin Catalytic Domain Protein  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Warner-Lambert Company  
STREET: 2800 Plymouth Rd.  
CITY: Ann Arbor  
STATE: MI

COUNTRY: US  
ZIP: 48105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/281,313  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/012,705  
FILING DATE: 03-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Tinney, Francis J.  
REGISTRATION NUMBER: 33,069  
REFERENCE/DOCKET NUMBER: 4415-01-FJT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 313 996-7295  
TELEFAX: 313 996-1553  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Thiolester-bond  
LOCATION: 3..4  
US-08-281-313-8

Query Match 67.7%; Score 21; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 Plg1 4  
1111  
Db 1 PLGL 4

RESULT 15  
US-09-101-167-18  
Sequence 18, Application US/09101167B  
Patent No. 6127139  
GENERAL INFORMATION:  
APPLICANT: TE KOPELE, Johannes M  
APPLICANT: BEERMAN, Bob  
TITLE OF INVENTION: METHOD FOR ASSAYING PROTEOLYTIC ENZYMES USING  
TITLE OF INVENTION: FLUORESCENCE-QUENCHED SUBSTRATES  
FILE REFERENCE: TE KOPELE et al. 09/101,167  
CURRENT APPLICATION NUMBER: US/09/101,167B  
CURRENT FILING DATE: 1998-07-02  
EARLIER APPLICATION NUMBER: EP 96200017.0  
EARLIER FILING DATE: 1996-01-04  
EARLIER APPLICATION NUMBER: PCT/NL97/00002  
EARLIER FILING DATE: 1997-01-02  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 18  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism:UNKNOWN  
US-09-101-167-18

Query Match 64.5%; Score 20; DB 3; Length 7;  
Best Local Similarity 57.1%; Pred. No. 1.6e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy	1	plglxar	7
	1	11	1:
Db	1	FOGLEAK	7

Search completed: March 1, 2002, 06:52:55  
Job time: 132 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2002, 06:47:48 ; Search time 12.96 Seconds  
(without alignments)  
41.144 Million cell updates/sec

Title: 09-876091-2  
Perfect score: 31  
Sequence: 1 p1g1xar 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR-68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	93.5	1201	2	A83007
2	29	93.5	1275	2	A38985
3	28	90.3	130	2	T49107
4	28	90.3	181	2	D75052
5	28	90.3	181	2	A71108
6	28	90.3	181	2	T44572
7	28	90.3	358	2	H83554
8	28	90.3	400	2	S54642
9	27	87.1	153	2	S73666
10	27	87.1	189	2	T30352
11	27	87.1	308	1	H65050
12	27	87.1	308	2	C85919
13	27	87.1	368	2	G82837
14	27	87.1	373	2	A83341
15	27	87.1	387	2	T38631
16	27	87.1	518	2	G75532
17	27	87.1	551	2	A83232
18	27	87.1	662	2	G82721
19	27	87.1	829	2	S58241
20	27	87.1	1646	1	WMTMS2
21	26	83.9	91	2	G81034
22	26	83.9	198	2	B82825
23	26	83.9	215	2	S61841
24	26	83.9	215	2	S61843
25	26	83.9	215	2	F81154
26	26	83.9	217	1	R1BSAP
27	26	83.9	217	2	J50492
28	26	83.9	218	2	S43016
29	26	83.9	273	1	S35647

30	26	83.9	331	2	C83701	hypothetical prote
31	26	83.9	358	2	F83831	spore germination
32	26	83.9	369	2	T50666	glutamate 5-K-kinase
33	26	83.9	371	2	D84186	hypothetical prote
34	26	83.9	440	2	F70792	hypothetical prote
35	26	83.9	473	2	D83508	two-component resp
36	26	83.9	508	1	ZUHUR	erythropoietin rec
37	26	83.9	525	2	T50893	methoxyneurosporen
38	26	83.9	700	2	D70951	probable UvrD - My
39	26	83.9	847	1	A53800	mixed-lineage prot
40	26	83.9	876	2	A45956	beta-glucosidase (
41	26	83.9	880	2	B45956	beta-glucosidase (
42	26	83.9	1451	2	I40325	dermonecrotic tox
43	26	83.9	3137	1	A37797	collagen alpha 3(V
44	25	80.6	72	2	A56376	chlorophyll a/b-bi
45	25	80.6	75	2	T06193	chlorophyll a/b-bi

## ALIGNMENTS

```

RESULT 1
A83007
Hypothetical protein PA5114 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: A83007
R:Stover, C.K.; Pham, X.Q.; Ervin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
  adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laidig, K.; L
  .; Lory, S.; Olson, M.V.
  Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82950; MUID:20437337
A:Accession: A83007
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1201 <STO>
A:Cross-references: GB:AE004924; GB:AE004091; NID:g9951407; PIDN:AAG08499.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA5114

Query Match          93.5%; Score 29; DB 2; Length 1201;
Best Local Similarity 85.7%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 p1g1xar 7
DB 488 PLGLDAR 494

RESULT 2
A38985
Nucleotide exchange factor CDC25 - human
N:Alternate names: Ras-specific guanine nucleotide-releasing factor
C:Species: Homo sapiens (man)
C:Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 05-Nov-1999
C:Accession: A38985; A46199; I58371
R:Wei, W.; Broek, D.
  submitted to GenBank, December 1994
A:Description: Cloning and analysis of the full length human cdc25 cDNA, a ras-specif
A:Reference number: A38985
A:Accession: A38985
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1275 <WEI>
A:Cross-references: GB:L26584; NID:9433719; PIDN:AAA58417.1; PID:9433720
R:Wei, W.; Moschler, R.D.; Sanyal, P.; Gonzales, E.; McKinney, D.; Dasgupta, C.; Li,
  Proc. Natl. Acad. Sci. U.S.A. 89, 7100-7104, 1992
A:Title: Identification of a mammalian gene structurally and functionally related to
A:Reference number: A46199; MUID:92357779
A:Accession: A46199

```

A:Molecule type: mRNA  
A:Residues: 1047-1054, 'A', 1056-1112, 'G', 1114-1135, 'C', 1137-1275 <WE2>  
A:Experimental source: brain  
A:Note: sequence extracted from NCBI backbone (NCBIN:111098, NCBIP:111099)  
R:Schweighofer, F.; Faure, M.; Fath, I.; Chevallerier-Multon, M.C.; Apion, F.; Dutrillaux  
Oncogene 8, 1477-1485, 1993  
A>Title: Identification of a human guanine nucleotide-releasing factor (H-GRF55) specific  
A:Reference number: 158371; MUID:93275641  
A:Accession: 158371  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 787-1275 <RES>  
A:Cross-references: GB:S62035; NID:9386046; PIDN:AB26881.1; PID:9386047  
C:Superfamily: CDC25-type guanine nucleotide exchange activator homology; CDC24 homology  
F:240-426/Domain: CDC24 homology <CD24>  
F:1036-1272/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>

Query Match 93.5%; Score 29; DB 2; Length 1275;  
Best Local Similarity 85.7%; Pred. No. 96;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 plglxar 7  
111111  
Db 14 PLGLAR 20

RESULT 3  
T49107  
hypothetical protein AT4g22000 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 18-Aug-2000  
C:Accession: T49107  
R:Bayan, M.; Medler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; M  
submitted to the Protein Sequence Database, May 2000  
A:Reference number: 225016  
A:Accession: T49107  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-130 <BEV>  
A:Cross-references: EMBL:AL022140; GSPDB:GN00062; ATSP:AT4g22000  
A:Experimental source: cultivar Columbia; BAC clone F1N20  
C:Genetics:  
A:Gene: ATSP:AT4g22000  
A:Map position: 4  
C:Superfamily: Arabidopsis thaliana hypothetical protein AT4g22000

Query Match 90.3%; Score 28; DB 2; Length 130;  
Best Local Similarity 71.4%; Pred. No. 16;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 plglxar 7  
111111  
Db 46 PLGISAR 52

RESULT 4  
D75052  
ribosomal protein L10 PAB1444 - Pyrococcus abyssi (strain Orsay)  
C:Species: Pyrococcus abyssi  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 18-Aug-2000  
C:Accession: D75052  
R:Anonymous; Genoscope  
submitted to the EMBL Data Library, July 1999  
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru  
A:Reference number: A75001  
A:Accession: D75052  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-181 <KAN>  
A:Cross-references: GB:AJ248287; GB:AL096836; NID:95458657; PIDN:CA850313.1; PID:9545882  
A:Experimental source: strain Orsay

C:Genetics:  
A:Gene: PAB1444  
C:Superfamily: rat ribosomal protein L10

Query Match 90.3%; Score 28; DB 2; Length 181;  
Best Local Similarity 71.4%; Pred. No. 22;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 plglxar 7  
111111  
Db 119 PLGLAR 125

RESULT 5  
A71108  
ribosomal protein L10 [similarity] - Pyrococcus horikoshii  
C:Species: Pyrococcus horikoshii  
C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 18-Aug-2000  
C:Accession: A71108  
R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Se  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu  
DNA Res. 5, 55-76, 1998  
A>Title: Complete sequence and gene organization of the genome of a hyper-thermophil  
A:Reference number: A71000; MUID:98344137  
A:Accession: A71108  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-181 <KAN>  
A:Cross-references: GB:AP000003; NID:93236130; PIDN:BA29723.1; PID:93257040  
A:Experimental source: strain Ors  
A:Note: this accession replaces an interim accession for a sequence replaced by GenBa  
C:Genetics:  
A:Gene: PH0633  
C:Superfamily: rat ribosomal protein L10

Query Match 90.3%; Score 28; DB 2; Length 181;  
Best Local Similarity 71.4%; Pred. No. 22;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 plglxar 7  
111111  
Db 119 PLGLAR 125

RESULT 6  
T44572  
ribosomal protein L10 [similarity] - Pyrococcus furiosus  
N:Alternate names: QM homolog  
C:Species: Pyrococcus furiosus  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 18-Aug-2000  
C:Accession: T44572  
R:Jenney Jr., F.E.; Verhagen, M.F.; Cui, X.; Adams, M.W.  
Science 286, 306-309, 1999  
A>Title: Anaerobic microbes: oxygen detoxification without superoxide dismutase.  
A:Reference number: 222794; MUID:99445924  
A:Accession: T44572  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-181 <JEN>  
A:Cross-references: EMBL:AF156097; NID:96066235; PIDN:AAF03230.1; PID:96066245  
C:Superfamily: rat ribosomal protein L10

Query Match 90.3%; Score 28; DB 2; Length 181;  
Best Local Similarity 71.4%; Pred. No. 22;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 plglxar 7  
111111  
Db 119 PLGLAR 125

```
RESULT 7
H83554
hypothetical protein PA0736 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: H83554
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
  adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
  ; Lory, S.; Olson, M.V
  Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
  A:Reference number: A82950; MUID:20437337
A:Accession: H83554
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STO>
A:Cross-references: GB:AE004508; GB:AE004091; NID:99946611; PIDN:AA604125.1; GSPDB:GN001
  A:Experimental source: strain PA01
  C:Genetics:
  A:Gene: PA0736

Query Match          90.3%; Score 28; DB 2; Length 358;
Best Local Similarity 71.4%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 plg1xar 7
    111111
Db 349 PLG1AAR 355

RESULT 8
S54642
glycine cleavage T protein GCVI - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein D3230; protein P2D400; protein YP9335.05c; protein YDR019c
C:Species: Saccharomyces cerevisiae
C>Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 17-Nov-2000
C:Accession: S54642; S63426; S67832; S72117; JG6309
R:Redman, K.; Brown, D.; Hamlyn, N.; Bowman, S.
  Submitted to the EMBL Data Library, May 1995
A:Reference number: S54638
A:Accession: S54642
A:Molecule type: DNA
A:Residues: 1-400 <DED>
A:Cross-references: EMBL:Z49770; NID:9840867; PIDN:CA89844.1; PID:9840872
A:Experimental source: strain AB972
R:Elide, L.G.; Sander, C.; Prydz, H.
  Submitted to the EMBL Data Library, February 1996
A:Description: Sequencing and analysis of a 35.4 kb region on the left arm of chromosome
  A:Reference number: S63416
A:Accession: S63426
A:Molecule type: DNA
A:Residues: 1-400 <EID>
A:Cross-references: EMBL:X95966; NID:91216215; PIDN:CAA65211.1; PID:91216226
R:Prydz, H.; Elide, L.G.
  Submitted to the Protein Sequence Database, July 1996
A:Reference number: S67822
A:Accession: S67832
A:Molecule type: DNA
A:Residues: 1-400 <PRY>
A:Cross-references: EMBL:Z74315; NID:91431445; PIDN:CAA98840.1; PID:91431446; MIPS:YDR01
  A:Experimental source: strain S288C
R:Elide, L.G.; Sander, C.; Prydz, H.
  Yeast 12, 1085-1090, 1996
A:Title: Sequencing and analysis of a 35.4 kb region on the left arm of chromosome IV fr
  A:Reference number: S72107; MUID:97051598
A:Accession: S72117
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-400 <ETW>
A:Cross-references: EMBL:X95966; NID:91216215; PIDN:CAA65211.1; PID:91216226
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
```

```
R:McNeill, J.B.; Zhang, F.; Taylor, B.V.; Sinclair, D.A.; Pearlman, R.E.; Bogner, A.L.
  Gene 186, 13-20, 1997
A:Title: Cloning, and molecular characterization of the GCVI gene encoding the glycine
  A:Reference number: JC6309; MUID:97199363
A:Accession: JC6309
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133; 'R', 135-261, 'T', 263-400 <MCN>
A:Genetics:
  A:Gene: SGD:GCVI
  A:Cross-references: MIPS:YDR019c; SGD:S0002426
  A:Map position: 4R
  C:Superfamily: aminomethyltransferase
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Query Match          90.3%; Score 28; DB 2; Length 400;
Best Local Similarity 71.4%; Pred. No. 51;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 plg1xar 7
    111111
Db 244 PLG1AAR 250
```

```
RESULT 9
S73666
adhesin P1 homolog P02_ORF153L - Mycoplasma pneumoniae (strain ATCC 29342)
C:Species: Mycoplasma pneumoniae
A:Varley, ATCC 29342
C>Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
C:Accession: S73666
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
  Nucleic Acids Res. 24, 4420-4449, 1996
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumon
  A:Reference number: S73327; MUID:97105885
A:Accession: S73666
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-153 <HTM>
A:Cross-references: EMBL:AE000032; GB:U00089; NID:91674011; PIDN:AA95993.1; PID:9167
  A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
  C:Genetics:
  A:Genetic code: SGC3
  A:Start codon: TTG
  C:Superfamily: Mycoplasma pneumoniae adhesin P1 homolog P02_ORF153L
```

```
Query Match          87.1%; Score 27; DB 2; Length 153;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 plg1xar 7
    111111
Db 70 PLGVAAR 76

RESULT 10
T30352
hypothetical protein ORF5 - Lymantria dispar nuclear polyhedrosis virus
C:Species: Lymantria dispar polyhedrosis virus, LdMNPV
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jul-2000
C:Accession: T30352
R:Kuzio, J.; Pearson, M.N.; Hatwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; R
  viology 253, 17-34, 1999
A:Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantri
  A:Reference number: Z20836; MUID:99124785
A:Accession: T30352
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-189 <KUZ>
A:Cross-references: EMBL:AF081810; NID:93822234; PIDN:AACT0190.1; PID:93822239
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Query Match 87.1%; Score 27; DB 2; Length 189;  
 Best Local Similarity 71.4%; Pred. No. 41;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglxar 7  
 ||| |  
 Db 179 PLGLAR 185

RESULT 11  
 H65050  
 Probable ATP-binding protein gntQ - Escherichia coli  
 C:Species: Escherichia coli  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 29-Sep-1999  
 C:Accession: H65050; A48429; S10373  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC  
 A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A:Title: The complete genome sequence of Escherichia coli K-12.  
 A:Reference number: A64720; MUID:97426617  
 A:Accession: H65050  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-308 <BLAT>  
 A:Cross-references: GB:AE000354; GB:U00096; NID:92367149; PIDN:AAC75750.1; PID:91789060;  
 A:Experimental source: strain K-12, substrain MG1655  
 R:Yamada, M.; Yamada, Y.; Sater Jr., M.H.  
 DNA Seq. 1, 141-145, 1990  
 A:Title: Nucleotide sequence and expression of the gntQ gene within the glucitol operon  
 A:Reference number: A48429; MUID:92190542  
 A:Accession: A48429  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-200, 'VN', 'R', '228', 'RD', '231', 'CDAGTQPH', '240', 'SCA', '244-246', 'W', <TAM>  
 A:Cross-references: EMBL:X51361; NID:941631; PIDN:CA35745.1; PID:941632  
 A:Note: sequence extracted from NCBI backbone (NCBIN:89668, NCBI:89670)  
 C:Genetics:  
 A:Gene: gntQ  
 A:Map position: 58 min  
 C:Superfamily: probable ATP-binding protein gntQ; CBS homology  
 C:Keywords: ATP

Query Match 87.1%; Score 27; DB 1; Length 308;  
 Best Local Similarity 71.4%; Pred. No. 68;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglxar 7  
 ||| |  
 Db 116 PLGLAK 122

RESULT 12  
 C85919  
 hypothetical protein gntQ [imported] - Escherichia coli (strain O157:H7)  
 C:Species: Escherichia coli  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 31-Mar-2001  
 C:Accession: C85919  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
 Miller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: C85919  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-308 <STO>  
 A:Cross-references: GB:AE005174; NID:912517153; PIDN:AG57815.1; GSPDB:GN00145; UWGP:240  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: gntQ

Query Match 87.1%; Score 27; DB 2; Length 308;  
 Best Local Similarity 71.4%; Pred. No. 68;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglxar 7  
 ||| |  
 Db 116 PLGLAK 122

RESULT 13  
 G82837  
 glycine cleavage T protein XF0183 [imported] - Xylella fastidiosa (strain 9a5c)  
 C:Species: Xylella fastidiosa  
 C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Sep-2000  
 C:Accession: G82837  
 R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq  
 Nature 406, 151-157, 2000  
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A:Reference number: A82515; MUID:20365717  
 A:Note: for a complete list of authors see reference number A59328 below  
 A:Accession: G82837  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-368 <SIM>  
 A:Cross-references: GB:AE003872; GB:AE003849; NID:99104975; PIDN:AAF82996.1; GSPDB:GN  
 A:Experimental source: strain 9a5c  
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.  
 Brites, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre  
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facinanzi, A.P.; Ferreira, A.J.S.  
 submitted to GenBank, June 2000  
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Fr  
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Klieger, J.E.; Kuramae, E.E.; La  
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins  
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.  
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,  
 Rodrigues, V.; Rosa, A.J.; de M., de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa  
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv  
 M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.  
 A:Reference number: A59328  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: XF0183  
 C:Superfamily: aminomethyltransferase

Query Match 87.1%; Score 27; DB 2; Length 368;  
 Best Local Similarity 71.4%; Pred. No. 81;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglxar 7  
 ||| |  
 Db 223 PLGLAR 229

RESULT 14  
 A83341  
 glycine cleavage system protein T2 PA2442 [imported] - Pseudomonas aeruginosa (strain  
 C:Species: Pseudomonas aeruginosa  
 C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C:Accession: A83341  
 R:Stover, C.K.; Plam, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;  
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; L  
 Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa  
 A:Reference number: A82950; MUID:20437337  
 A:Accession: A83341  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-573 <STO>  
 A:Cross-references: GB:AE004671; GB:AE004091; NID:9948483; PIDN:AG05830.1; GSPDB:GN  
 A:Experimental source: strain PA01  
 C:Genetics:

A:Gene: gcvT2; PA2442  
C:Superfamily: aminomethyltransferase

Query Match 87.1%; Score 27; DB 2; Length 373;  
Best Local Similarity 71.4%; Pred. No. 82;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 plglxar 7  
1:11111  
Db 221 PIGLGAR 227

RESULT 15

T38631  
aminomethyltransferase precursor - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jan-2000  
C:Accession: T38631  
R:McLean, J.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, September 1997  
A:Reference number: Z21722  
A:Accession: T38631  
A:Status: preliminary; translated from GR/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-387 <MCL>  
A:Cross-references: EMBL:Z98979; PIDN:CA811698.1; GSPDB:GN00066; SPDB:SPAC31G5.14  
A:Experimental source: strain 972h; cosmid c31G5  
C:Genetics:  
A:Gene: SPDB:SPAC31G5.14  
A:Map position: 1  
C:Superfamily: aminomethyltransferase

Query Match 87.1%; Score 27; DB 2; Length 387;  
Best Local Similarity 71.4%; Pred. No. 86;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 plglxar 7  
1:11111  
Db 242 PIGLGAR 248

Search completed: March 1, 2002, 06:48:11  
job time: 23 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2002, 06:48:33 ; Search time 10.16 Seconds  
(without alignments)  
25.261 Million cell updates/sec

Title: 09-876091-2  
Perfect score: 31  
Sequence: 1 p1g1xar 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues  
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	93.5	1275	1 GNRP_HUMAN	Q13972 homo sapien
2	28	90.3	181	1 RL10_PIRAB	Q3uy99 pyrococcus
3	28	90.3	181	1 RL10_PYRHO	O58363 pyrococcus
4	28	90.3	400	1 GCST_YEAST	P48015 saccharomyc
5	27	87.1	321	1 GUT0_ECOLI	P17115 escherichia
6	27	87.1	368	1 GCST_XYLFA	O9p9w5 xyllella fas
7	27	87.1	387	1 GCST_SCHPO	O44110 schizosacch
8	27	87.1	829	1 PQOF_PSEFL	P51743 pseudomonas
9	27	87.1	1648	1 RRPO_CGNVS	P19523 cucumber gr
10	26	83.9	174	1 KAD_NEIAC	O59591 neisseria c
11	26	83.9	174	1 KAD_NEIIC	O59594 neisseria c
12	26	83.9	174	1 KAD_NEIFL	O59596 neisseria f
13	26	83.9	174	1 KAD_NEIHA	O59615 neisseria l
14	26	83.9	215	1 KAD_NEIHP	O59618 neisseria p
15	26	83.9	215	1 KAD_NEIHO	P49979 neisseria g
16	26	83.9	215	1 KAD_NEIMA	P49980 neisseria m
17	26	83.9	215	1 KAD_NEIMU	P49981 neisseria m
18	26	83.9	217	1 KAD_BACST	P27142 bacillus st
19	26	83.9	217	1 KAD_BACSU	P16304 bacillus su
20	26	83.9	218	1 KAD_BORPE	P39068 bordetella
21	26	83.9	218	1 MT1B_MORBO	P47421 moraxella b
22	26	83.9	369	1 PROB_CORGL	P46546 corynebacte
23	26	83.9	508	1 EPRO_HUMAN	P19235 homo sapien
24	26	83.9	700	1 UVRD_MYCTU	O53344 mycobacteri
25	26	83.9	876	1 BGL1_SACFI	P22506 saccharomyc
26	26	83.9	880	1 BGL2_SACFI	P22507 saccharomyc
27	26	83.9	3137	1 CA36_CHICK	P15969 gallus gall
28	26	80.6	220	1 TPIS_CHLAU	P66744 chlocofleux
29	25	80.6	266	1 CB21_MHEAT	P4784 triticum ae
30	25	80.6	270	1 GPRL_YARLI	P41943 yarowia li
31	25	80.6	283	1 YCQO_YEAST	P25613 saccharomyc
32	25	80.6	304	1 YDEQ_ECOLI	P7388 escherichia
33	25	80.6	314	1 YG2O_YEAST	P53257 saccharomyc

## ALIGNMENTS

34	25	80.6	328	1 TEHA_HAEN	P44741 haemophilus
35	25	80.6	336	1 PYRD_ECOLI	P05021 escherichia
36	25	80.6	336	1 PYRD_SALTY	P25468 salmonella
37	25	80.6	351	1 PYRD_HELPJ	O92m11 helicobacte
38	25	80.6	351	1 PYRD_HELPJ	O25655 helicobacte
39	25	80.6	356	1 PYRD_MYCLE	P46727 mycobacteri
40	25	80.6	357	1 PYRD_MYCTU	O06236 mycobacteri
41	25	80.6	369	1 PYRD_DEIRA	O9rx14 delnococcus
42	25	80.6	376	1 PROB_MYCTU	P71910 mycobacteri
43	25	80.6	392	1 GCST_CHICK	P28337 gallus gall
44	25	80.6	430	1 NOR2_RAT	O63516 rattus norv
45	25	80.6	432	1 SHH_CYNPY	O90385 cynops pyrr

RESULT 1	GNRP_HUMAN	STANDARD;	PRT; 1275 AA.
ID	GNRP_HUMAN		
AC	Q13972;		
DT	20-AUG-2001 (Rel. 40, Created)		
DT	20-AUG-2001 (Rel. 40, Last sequence update)		
DE	GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP) (RAS-SPECIFIC NUCLEOTIDE		
DE	EXCHANGE FACTOR CDC25).		
GN	RASGRP1 OR CDC25.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCHI_Taxid=9606;		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RA	Wei W., Brock D.;		
RT	"Cloning and analysis of the full length human cdc25 cDNA, a ras-		
RT	specific nucleotide exchange factor.";		
RL	Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.		
CC	-1- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP.		
CC	-1- SIMILARITY: CONTAINS 2 PH DOMAINS.		
CC	-1- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).		
CC	-1- SIMILARITY: CONTAINS 1 RASGEF DOMAIN.		
CC	-1- SIMILARITY: CONTAINS 1 IQ DOMAIN.		
CC	-----		
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).		
CC	-----		
DR	EMBL; L26584; AAA58417.1; -		
DR	InterPro; IPR001331; GDS_CDC24.		
DR	InterPro; IPR000048; IQ.		
DR	InterPro; IPR001849; PH.		
DR	InterPro; IPR000651; RASGEFN.		
DR	InterPro; IPR001895; RASGEF_CDC25.		
DR	InterPro; IPR000219; RHOGEF.		
DR	Pfam; PF00612; IQ; 1.		
DR	Pfam; PF00169; PH; 2.		
DR	Pfam; PF00617; RASGEF; 1.		
DR	Pfam; PF00618; RASGEFN; 1.		
DR	Pfam; PF00621; RHOGEF; 1.		
DR	SMART; SM00015; IQ; 1.		
DR	SMART; SM00233; PH; 2.		
DR	SMART; SM00147; RASGEF; 1.		
DR	SMART; SM00229; RASGEFN; 2.		
DR	SMART; SM00325; RHOGEF; 1.		
DR	PROSITE; PS00720; GDS_CDC25; 1.		
DR	PROSITE; PS00741; GDS_CDC24; 1.		
DR	PROSITE; PSS0003; PH_DOMAIN; 2.		
DR	PROSITE; PSS0096; IQ; 1.		
DR	Guanine-nucleotide releasing factor.		

FT DOMAIN 22 129 PH 1.  
 FT DOMAIN 204 229 IO.  
 FT DOMAIN 247 431 DH.  
 FT DOMAIN 467 584 PH 2.  
 FT DOMAIN 1058 1272 RASGEF.  
 SQ SEQUENCE 1275 AA; 145381 MW; 86C6F54A1E451F1 CRC64;

Query Match 93.5%; Score 29; DB 1; Length 1275;  
 Best Local Similarity 85.7%; Pred. No. 51;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 p1glxar 7  
 |||||  
 Db 14 P1GLLAR 20

RESULT 2  
 RL10\_PYPAB STANDARD; PRT; 181 AA.  
 AC 09UYU9;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE 50S RIBOSOMAL PROTEIN L10E.  
 GN RPL10E OR PAB1444.  
 OS Pyrococcus abyssi.  
 OC Archaea; Euryarchaeota; Thermococcales; Pyrococcus.  
 OX NCBI\_TaxID=29292;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ORSAY;  
 RA Hellig R.;  
 RT "Pyrococcus abyssi genome sequence: Insights into archaeal chromosome structure and evolution."  
 RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE L10E FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----  
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 CC -----  
 CC EMBL: AJ248287; CAB50313.1;  
 DR InterPro: IPR001197; Ribosomal\_L10E.  
 DR Pfam: PF00826; Ribosomal\_L10E; 1.  
 DR PROSITE: PS01257; RIBOSOMAL\_L10E; FALSE\_NEG.  
 KW Ribosomal protein; Complete proteome.  
 SQ SEQUENCE 181 AA; 20884 MW; 055C3764DC9806B CRC64;

Query Match 90.3%; Score 28; DB 1; Length 181;  
 Best Local Similarity 71.4%; Pred. No. 15;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 p1glxar 7  
 |||||  
 Db 119 P1GLLAR 125

RESULT 3  
 RL10\_PYPAB STANDARD; PRT; 181 AA.  
 AC 058367;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE 50S RIBOSOMAL PROTEIN L10E.  
 GN RPL10E OR PH0633 OR PHAE019.  
 OS Pyrococcus horikoshii.

OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.  
 OX NCBI\_TaxID=53953;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OT3;  
 RX MEDLINE=98344137; PubMed=9679194;  
 RA Kawarabayashi Y., Sawada M., Horikawa H., Halkawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.;  
 RT "Complete sequence and gene organization of the genome of a hyper-thermophilic archaeobacterium, Pyrococcus horikoshii OT3."  
 RL DNA Res. 5:55-76(1998).  
 CC -1- SIMILARITY: BELONGS TO THE L10E FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----  
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 CC -----  
 CC EMBL: AP000003; BAA29723.1;  
 DR InterPro: IPR001197; Ribosomal\_L10E.  
 DR Pfam: PF00826; Ribosomal\_L10E; 1.  
 DR PROSITE: PS01257; RIBOSOMAL\_L10E; FALSE\_NEG.  
 KW Ribosomal protein; Complete proteome.  
 SQ SEQUENCE 181 AA; 20917 MW; E9179A3BAF6A001E CRC64;

Query Match 90.3%; Score 28; DB 1; Length 181;  
 Best Local Similarity 71.4%; Pred. No. 15;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 p1glxar 7  
 |||||  
 Db 119 P1GLLAR 125

RESULT 4  
 GCST\_YEAST STANDARD; PRT; 400 AA.  
 AC P48015;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE AMINOMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (PC 2.1.2.10) (GLYCINE CLEAVAGE SYSTEM T PROTEIN) (GCVT).  
 GN GCY1 OR YDR019C OR YD9335.05C.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes.  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9719363; PubMed=9047339;  
 RA McNeil J.B., Zhang F.R., Taylor B.V., Pearlman R.E., Bogner A.L.;  
 RT "Cloning, and molecular characterization of the GCY1 gene encoding the glycine cleavage T-protein from Saccharomyces cerevisiae."  
 RL Gene 186:13-20(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C / AB972;  
 RA Dedman K., Brown D., Hamlyn N., Bowman S., Barrell B.G., Rajandream M.A.;  
 RL Submitted (MAY-1995) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97051598; PubMed=8896275;  
 RA Elde L.G., Sander C., Prydz H.;



"Sequencing and analysis of a 35.4 kb region on the right arm of RT chromosome IV from *Saccharomyces cerevisiae* reveal 23 open reading frames.";  
 RL Yeast 12:1085-1090(1996).  
 CC -1- FUNCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYZES THE DEGRADATION OF GLYCINE.  
 CC -1- CATALYTIC ACTIVITY: (6S)-TETRAHYDROFOLATE + S-AMINOMETHYLDIHYDROLIPOYLPROTEIN - (6R)-5,10-METHYLENTERAHYDROFOLATE + NH(3) + DIHYDROLIPOYLPROTEIN.  
 CC SUBUNIT: THE GLYCINE CLEAVAGE SYSTEM IS COMPOSED OF FOUR PROTEINS: P, T, L, AND H.  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.  
 CC -1- SIMILARITY: BELONGS TO THE GCVT FAMILY.  
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 CC -----  
 DR EMBL: LA1522; AAB05000.1; -;  
 DR EMBL: Z49770; CAAB9844.1; -;  
 DR EMBL: X95966; CAAB5211.1; -;  
 DR EMBL: Z74315; CAAB9840.1; -;  
 DR SGD: S0002426; GCVL.  
 DR InterPro: IPR002536; GCV\_T.  
 DR Pfam: PF01571; GCV\_T; 1.  
 DR Transferrase: Aminotransferase; Mitochondrion; Transit peptide.  
 FT TRANSIT 1 ? MITOCHONDRION (POTENTIAL).  
 FT CHAIN ? 400 AMINOMETHYLTRANSFERASE.  
 FT CONFLICT 122 122 D -> E (IN REF. 1).  
 SQ SEQUENCE 400 AA; 44469 MW; FFA349B0E0176D5 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 400;  
 Best Local Similarity 71.4%; Pred. No. 31;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 pligixar 7  
 1:1111  
 DB 244 PIGLAAR 250

RESULT 5  
 GUTQ\_ECOLI STANDARD; PRT; 321 AA.  
 AC P17115; Q46874;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE GUTQ PROTEIN.  
 GN GUTQ OR SRLQ OR B2708.  
 OS *Escherichia coli*.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; *Escherichia*.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE OF 3-313 FROM N.A.  
 RC STRAIN=K12;  
 RA MEDLINE=92190542; PubMed=2134185;  
 RA Yamada M., Yamada Y., Sailer M.H. Jr.;  
 RT "Nucleotide sequence and expression of the gutQ gene within the gluctol operon of *Escherichia coli*.";  
 RL DNA Seq. 1:141-145(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RA MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;  
 RT "The complete genome sequence of *Escherichia coli* K-12.";  
 RL Science 277:1453-1474(1997).  
 CC -1- FUNCTION: NOT KNOWN.  
 CC -1- SUBUNIT: HOMODIMER (POSSIBLE).  
 CC -1- SIMILARITY: BELONGS TO THE SIS FAMILY. GUTQ/KPSF SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.  
 CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 214.  
 CC -----  
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 CC -----  
 DR EMBL: X51361; CAAB3745.1; ALT\_FRAME.  
 DR EMBL: U29579; AAA69217.1; ALT\_INIT.  
 DR EMBL: AE000354; AAC75750.1; ALT\_INIT.  
 DR PIR: S10373; S10373.  
 DR PIR: A48429; A48429.  
 DR EcoGene: EG10973; gutQ.  
 DR InterPro: IPR000644; CBS.  
 DR InterPro: IPR001347; SIS.  
 DR Pfam: PF00571; CBS; 2.  
 DR Pfam: PF01380; SIS; 1.  
 DR ATP-binding; Repeat; CBS domain; Complete proteome.  
 FT NP\_BIND 49 54 ATP (POTENTIAL).  
 FT DOMAIN 201 255 CBS 1.  
 FT DOMAIN 267 319 CBS 2.  
 SQ SEQUENCE 321 AA; 34031 MW; 85C31DFBD92F7B7C CRC64;

Query Match 87.1%; Score 27; DB 1; Length 321;  
 Best Local Similarity 71.4%; Pred. No. 43;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 pligixar 7  
 111111  
 DB 129 PIGLAAR 135

RESULT 6  
 GCST\_XYLFRA STANDARD; PRT; 368 AA.  
 ID GCST\_XYLFRA  
 AC Q9PGW5;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE PROBABLE AMINOMETHYLTRANSFERASE (EC 2.1.2.10) (GLYCINE CLEAVAGE SYSTEM T PROTEIN).  
 GN GCVT OR XF0183.  
 OS *Xyella fastidiosa*.  
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group; *Xyella*.  
 OX NCBI\_TaxID=2371;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=9A5C;  
 RX MEDLINE=20365717; PubMed=10910347;  
 RA Simpson A.J.G., Reinhard F.C., Arruda P., Abreu F.A., Acencio M., Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H., Coutinho L.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M., Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H., Facinanci A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kita[uma] J.P., Krieger J.E., Kuramae E.E., Laligret F., Lambais M.R., Leite L.C.C.,

RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,  
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,  
 RA Mench M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,  
 RA Mench C.F.H., Miracca E.C., Miyaki C.T., Monteiro-Vitollo C.B.,  
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,  
 RA Nohai A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,  
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,  
 RA Peloto B.R., Pereira G.A.G., Pereira H.A.Jr., Pesquero J.B.,  
 RA Quagato R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,  
 RA de Rosa V.E. Jr., de Sa R.G., Sanceli R.V., Sawasaki H.E.,  
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,  
 RA da Silveira J.F., Silvestri M.L.Z., Silveira W.J., de Souza A.A.,  
 RA de Souza A.P., Terenzi M.F., Trufi D., Tsai S.M., Tsubako M.H.,  
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,  
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.,  
 RT "The genome sequence of the plant pathogen *Xylella fastidiosa*,"  
 RL Nature 406:151-159(2000).  
 CC -1- FUNCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYZES THE DEGRADATION OF  
 CC GLYCINE (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: (6S)-TETRAHYDROFLATE +  
 CC S-AMINOMETHYLHYDROLYPOLPROTEIN = (6R)-5,10-  
 CC METHYLENETETRAHYDROFLATE + NH(3) + DIHYDROLIPOLPROTEIN.  
 CC -1- SUBUNIT: THE GLYCINE CLEAVAGE SYSTEM IS COMPOSED OF FOUR PROTEINS:  
 CC P, T, L, AND H (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE GCVT FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AE003872; AAF8296.1; -  
 DR InterPro: IPR002536; GCV\_T.  
 DR Pfam: PF01571; GCV\_T; 1.  
 KW Transferase: Aminotransferase; Complete proteome.  
 SO SEQUENCE 368 AA; 41148 MW; 1BDB7B6D265F78CF CRC64;

Query Match 87.1%; Score 27; DB 1; Length 368;  
 Best Local Similarity 71.4%; Pred. No. 49;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 piglxar 7  
 1:111111  
 Db 223 piglxar 229

RESULT 7  
 GCST\_SCHPO STANDARD; PRT; 387 AA.  
 AC 014110; Q92364;  
 DT 20-AUG-2001 (Rel. 40; Created)  
 DT 20-AUG-2001 (Rel. 40; Last sequence update)  
 DT 20-AUG-2001 (Rel. 40; Last annotation update)  
 DE PROBABLE AMINOMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.1.2.10)  
 DE (GLYCINE CLEAVAGE SYSTEM T PROTEIN) (GCVT).  
 GN SPAC3165.14 OR N313.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomyces.  
 CX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Nagao K., Arioka M., Kadokura H., Yoda K., Yamasaki M.;  
 RT "The nucleotide sequence of a 9.1 kb DNA fragment of  
 RT Schizosaccharomyces pombe chromosome reveals the presence of  
 RT pad1+/skst1+ gene and three previously unknown open reading frames,"  
 RL Submitted (Aug-1996) to the EMBL/Genbank/DBJ databases.  
 [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RL McLean J., Harris D., Barrell B.G., Rajandream M.A., Wood V.;  
 RL Submitted (SEP-1997) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYZES THE DEGRADATION OF  
 CC GLYCINE (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: (6S)-TETRAHYDROFLATE +  
 CC S-AMINOMETHYLHYDROLYPOLPROTEIN = (6R)-5,10-  
 CC METHYLENETETRAHYDROFLATE + NH(3) + DIHYDROLIPOLPROTEIN.  
 CC -1- SUBUNIT: THE GLYCINE CLEAVAGE SYSTEM IS COMPOSED OF FOUR PROTEINS:  
 CC P, T, L, AND H (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE GCVT FAMILY.  
 CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 305  
 CC ONWARD DUE TO A FRAMESHIFT.  
 CC -----  
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 CC -----  
 DR EMBL: D84656; BAA12709.1; ALT\_FRAME.  
 DR EMBL: Z98979; CAB11698.1; -  
 DR InterPro: IPR002536; GCV\_T.  
 DR Pfam: PF01571; GCV\_T; 1.  
 KW Transferase: Aminotransferase; Mitochondrion; Transit peptide.  
 FT TRANSIT 1 ?  
 FT CHAIN 127 387 MITOCHONDRIAL (POTENTIAL).  
 FT CHAIN 127 387 PROBABLE AMINOMETHYLTRANSFERASE.  
 FT CONFLICT 127 127 E -> G (IN REF. 1).  
 FT CONFLICT 255 255 A -> S (IN REF. 1).  
 FT CONFLICT 257 261 MCLYG -> NNAFME (IN REF. 1).  
 FT CONFLICT 264 264 I -> T (IN REF. 1).  
 SO SEQUENCE 387 AA; 42408 MW; 68A3CDBCF84C45A CRC64;

Query Match 87.1%; Score 27; DB 1; Length 387;  
 Best Local Similarity 71.4%; Pred. No. 51;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 piglxar 7  
 1:111111  
 Db 242 piglxar 248

RESULT 8  
 POOF\_PSEFL STANDARD; PRT; 829 AA.  
 AC P55174;  
 DT 01-OCT-1996 (Rel. 34; Created)  
 DT 01-OCT-1996 (Rel. 34; Last sequence update)  
 DT 01-OCT-1996 (Rel. 34; Last annotation update)  
 DE COENZYME PQQ SYNTHESIS PROTEIN F (EC 3.4.99.-).  
 GN POOF.  
 OS Pseudomonas fluorescens.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Pseudomonas.  
 CX NCBI\_TaxID=294;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=CHA0;  
 RX MEDLINE=96064397; PubMed=8526497;  
 RA Schindler U., Keel C., Defago G., Haas D.;  
 RT "Tn5-directed cloning of pqq genes from Pseudomonas fluorescens CHA0:  
 RT mutational inactivation of the genes results in overproduction of the  
 RT antibiotic polyleucin.",  
 RL Appl. Environ. Microbiol. 61:3856-3864(1995).  
 CC -1- FUNCTION: REQUIRED FOR COENZYME PYROLO-QUINOLINE-QUINONE (PQQ)  
 CC BIOSYNTHESIS. IT IS THOUGHT THAT THIS PROTEIN IS A PROTEASE THAT  
 CC CLEAVES PEPTIDES BOND IN A SMALL PEPTIDE (GENE PQA) WHICH WOULD  
 CC PROVIDE THE GLUTAMATE AND TYROSINE RESIDUES WHICH ARE NECESSARY

```
CC      FOR THE SYNTHESIS OF POQ (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M16; ALSO KNOWN AS THE
CC      INSULINASE FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: X87299; CAA60730.1; -.
CC      DR MEROPS: M16.006; -.
CC      DR InterPro: IPR001431; Peptidase M16.
CC      DR Pfam: PF00675; Peptidase M16.
CC      DR PROSITE, PS00143; INSULINASE. 1.
CC      KW POQ: Hydrolase; Metalloprotease; Zinc.
CC      FT METAL 62 62 ZINC (BY SIMILARITY).
CC      FT ACT_SITE 65 65 BY SIMILARITY.
CC      FT METAL 66 66 ZINC (BY SIMILARITY).
CC      FT METAL 143 143 ZINC (BY SIMILARITY).
CC      SQ SEQUENCE 829 AA; 91347 MW; 35F8A4AA9FDC1E6 CRC64;

Query Match      87.1%; Score 27; DB 1; Length 829;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy      1 piglxar 7
        1:1111
Db      487 PIGLHAR 493

RESULT 9
RRPO_CGVNS STANDARD; PRT; 1648 AA.
ID RRPO_CGVNS
AC P19523; Q83208; P89877; P90356;
DT 01-FEB-1991 (Rel. 17, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (186 KDA PROTEIN) [CONTAINS:
DE METHYLTRANSFERASE/RNA HELICASE (MT/HEL) (129 KDA PROTEIN)].
DE Cucumbr green mottle virus (watermelon strain SH) (CGMV), and
OS Cucumbr green mottle mosaic virus (watermelon strain W) (CGMV).
OC Viruses: ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
OX NCBI_TaxID=12236, 12237;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=SH;
RX MEDLINE=91311400; PubMed=1856687;
RA Ueki M., Tomiyama M., Kakutani T., Hidaka S., Kiguchi T., Nagata R.,
RA Sato T., Motoyoshi F., Nishiguchi M.;
RT "The complete nucleotide sequence of cucumber green mottle mosaic
RT virus (SH strain) genomic RNA."
RL J. Gen. Virol. 72:1487-1495(1991).
RN
RP REVISIONS.
RC STRAIN=SH;
RA Ueki M., Tomiyama M., Kakutani T., Hidaka S., Kiguchi T., Nagata R.,
RA Sato T., Motoyoshi F., Nishiguchi M.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE OF 1496-1648 FROM N.A.
RC STRAIN=W;
RX MEDLINE=89073773; PubMed=3201760;
RA Saito T., Imai Y., Meshi T., Okada Y.;
RT "Interviral homologues of the 30k proteins of tobamoviruses.";
RL Virology 167:653-656(1988).
CC -1- FUNCTION: THE LONGER PROTEIN IS A RNA POLYMERASE ACTIVE IN VIRAL
CC RNA REPLICATION.
CC -1- FUNCTION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA
CC CAPPING AND AN RNA HELICASE.
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CC      -1- MISCELLANEOUS: READTHROUGH OF THE TERMINATOR UAG OCCURS BETWEEN
CC      CODONS FOR LYS-1144 AND GLN-1146.
CC      -----
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CC      -----
CC      EMBL: D12505; BAA18895.1; -.
CC      DR EMBL: D12505; BAA18896.1; -.
CC      DR EMBL: J04322; AAA46382.1; -.
CC      DR PIR: J01157; WMTMS2.
CC      DR InterPro: IPR001788; RNA_dep_RNAPol2.
CC      DR InterPro: IPR002588; V_methyltransf.
CC      DR InterPro: IPR000606; Viral_helicel.
CC      DR Pfam: PF00978; RNA_dep_RNAPol2; 1.
CC      DR Pfam: PF01443; Viral_helicase1; 1.
CC      DR Pfam: PF01660; Viral_helicase1; 1.
CC      KW Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
CC      FT CHAIN 1 1648 RNA-DIRECTED RNA POLYMERASE.
CC      FT CHAIN 1 1144 METHYLTRANSFERASE/RNA HELICASE.
CC      FT NP_BIND 863 870 ATP (POTENTIAL).
CC      SQ SEQUENCE 1648 AA; 186549 MW; 1D1AFEEEB7B65595 CRC64;

Query Match      87.1%; Score 27; DB 1; Length 1648;
Best Local Similarity 71.4%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy      1 piglxar 7
        1:1111
Db      1087 PIGLHAR 1093

RESULT 10
KAD_NEIAN STANDARD; PRT; 174 AA.
ID KAD_NEIAN
AC Q59591;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADENYLATE KINASE (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE) (FRAGMENT).
GN ADK
OS Neisseria animalis.
OC Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=492;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=NCYC 10212;
RX MEDLINE=97149032; PubMed=8995060;
RA Fell E., Zhou J., Maynard Smith J., Spratt B.G.;
RT "A comparison of the nucleotide sequences of the adk and recA genes
RT of pathogenic and commensal Neisseria species: evidence for extensive
RT interspecies recombination within adk."
RL J. Mol. Evol. 43:631-640(1996).
RN
RP -1- FUNCTION: THIS SMALL UBQUITOUS ENZYME IS ESSENTIAL FOR
RP MAINTENANCE AND CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC      -----
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```

DR EMBL: U57713; AAB49184.1; -.  
 DR HSSP: P05082; 2ECK.  
 DR InterPro: IPR000850; Adenylate\_kin.  
 DR Pfam: PF00406; adenylatekinase.1.  
 DR ProDom: PD000657; Adenylate\_kin; 1.  
 DR PROSITE: PS00113; ADENYLATE\_KINASE; 1.  
 KW transferase; kinase; ATP-binding.  
 FT NON\_TER 1  
 FT NON\_TER 174  
 SQ SEQUENCE 174 AA; 19024 MW; 137DB65125AABFCD CRC64;

Query Match  
 Best Local Similarity 83.9%; Score 26; DB 1; Length 174;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 pliglar 7  
 DB 26 PUGLEAK 32

RESULT 11  
 KAD\_NEICI STANDARD: PRT; 174 AA.  
 AC Q59594;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE ADENYLATE KINASE (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE) (FRAGMENT).  
 GN ADK.  
 OS Neisseria clonerea.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=483;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LNP 1646;  
 RX MEDLINE-97149032; PubMed-8995060;  
 RA Fell E., Zhou J., Maynard Smith J., Spratt B.G.;  
 RT "A comparison of the nucleotide sequences of the adk and recA genes of pathogenic and commensal Neisseria species: evidence for extensive interspecies recombination within adk."  
 RL J. Mol. Evol. 43:631-640(1996).  
 CC -!- FUNCTION: THIS SMALL UBICUITOUS ENZYME IS ESSENTIAL FOR MAINTENANCE AND CELL GROWTH.  
 CC -!- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -!- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: U57710; AAB49185.1; -.  
 DR HSSP: P05082; 2ECK.  
 DR InterPro: IPR000850; Adenylate\_kin.  
 DR Pfam: PF00406; adenylatekinase.1.  
 DR ProDom: PD000657; Adenylate\_kin; 1.  
 DR PROSITE: PS00113; ADENYLATE\_KINASE; 1.  
 KW transferase; kinase; ATP-binding.  
 FT NON\_TER 1  
 FT NON\_TER 174  
 SQ SEQUENCE 174 AA; 19213 MW; DA13D118A59956B5 CRC64;

Query Match  
 Best Local Similarity 83.9%; Score 26; DB 1; Length 174;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 pliglar 7  
 DB 26 PUGLEAK 32

RESULT 12  
 KAD\_NEIFL STANDARD: PRT; 174 AA.  
 AC Q59596;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE ADENYLATE KINASE (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE) (FRAGMENT).  
 GN ADK.  
 OS Neisseria flavescens.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=484;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LNP 444;  
 RX MEDLINE-97149032; PubMed-8995060;  
 RA Fell E., Zhou J., Maynard Smith J., Spratt B.G.;  
 RT "A comparison of the nucleotide sequences of the adk and recA genes of pathogenic and commensal Neisseria species: evidence for extensive interspecies recombination within adk."  
 RL J. Mol. Evol. 43:631-640(1996).  
 CC -!- FUNCTION: THIS SMALL UBICUITOUS ENZYME IS ESSENTIAL FOR MAINTENANCE AND CELL GROWTH.  
 CC -!- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.  
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -!- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: U57711; AAB49186.1; -.  
 DR HSSP: P05082; 2ECK.  
 DR InterPro: IPR000850; Adenylate\_kin.  
 DR Pfam: PF00406; adenylatekinase.1.  
 DR ProDom: PD000657; Adenylate\_kin; 1.  
 DR PROSITE: PS00113; ADENYLATE\_KINASE; 1.  
 KW transferase; kinase; ATP-binding.  
 FT NON\_TER 1  
 FT NON\_TER 174  
 SQ SEQUENCE 174 AA; 19137 MW; F0886FE8F05C0FBB CRC64;

Query Match  
 Best Local Similarity 83.9%; Score 26; DB 1; Length 174;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 pliglar 7  
 DB 26 PUGLEAK 32

RESULT 13  
 KAD\_NEILA STANDARD: PRT; 174 AA.  
 AC Q59615;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE ADENYLATE KINASE (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE) (FRAGMENT).  
 GN ADK.  
 OS Neisseria lactamica.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

```

OX NCBI_TaxID=486;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCYC 10617;
RX MEDLINE=97149032; PubMed=8995060;
RA Fell E., Zhou J., Maynard Smith J., Spratt B.G.;
RT "A comparison of the nucleotide sequences of the adh and recA genes
RT of pathogenic and commensal Neisseria species: evidence for extensive
RT interspecies recombination within adh.";
RL J. Mol. Evol. 43:631-640(1996).
CC -1- FUNCTION: THIS SMALL UBICUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC -----
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CC -----
DR EMBL; U57709; AAB49187.1; -.
DR HSSP; P05082; 2ECK.
DR InterPro; IPR000850; Adenylate_kin.
DR Pfam; PF00406; adenylatekinase; 1.
DR ProDom; PD000657; Adenylate_kin; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
KW Transferase; Kinase; ATP-binding.
FT NON_TER 1 174
FT SEQUENCE 174 AA; 19155 MW; F622A9479A9AA57B CRC64;
SQ
Query Match 83.9%; Score 26; DB 1; Length 174;
Best Local Similarity 71.4%; Pred. No. 43;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 plg1xar 7
Db 26 PUGLEAK 32
RESULT 14
KAD_NEIPH STANDARD; PRT; 174 AA.
AC Q059628;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADENYLATE KINASE (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE) (FRAGMENT).
GN ADK.
OS Neisseria pharyngis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=29434;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCYC 4590 / FLAVA;
RX MEDLINE=97149032; PubMed=8995060;
RA Fell E., Zhou J., Maynard Smith J., Spratt B.G.;
RT "A comparison of the nucleotide sequences of the adh and recA genes
RT of pathogenic and commensal Neisseria species: evidence for extensive
RT interspecies recombination within adh.";
RL J. Mol. Evol. 43:631-640(1996).
CC -1- FUNCTION: THIS SMALL UBICUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U57712; AAB49189.1; -.
DR HSSP; P05082; 2ECK.
DR InterPro; IPR000850; Adenylate_kin.
DR Pfam; PF00406; adenylatekinase; 1.
DR ProDom; PD000657; Adenylate_kin; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
KW Transferase; Kinase; ATP-binding.
FT NON_TER 1 174
FT SEQUENCE 174 AA; 19155 MW; F622A9479A9AA57B CRC64;
SQ
Query Match 83.9%; Score 26; DB 1; Length 174;
Best Local Similarity 71.4%; Pred. No. 43;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 1 plg1xar 7
Db 26 PUGLEAK 32
RESULT 15
KAD_NEIGO STANDARD; PRT; 215 AA.
AC P49379;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADENYLATE KINASE (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE).
GN ADK.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CH-95;
RX MEDLINE=95349386; PubMed=7623557;
RA Vazquez J.A., Berron S., O'Rourke M., Carpenter G., Feil E.,
RA Smith N.H., Spratt B.G.;
RT "Interspecies recombination in nature: a meningococcus that has
RT acquired a gonococcal PIB porin.";
RL Mol. Microbiol. 15:1001-1007(1995).
CC -1- FUNCTION: THIS SMALL UBICUITOUS ENZYME IS ESSENTIAL FOR
CC MAINTENANCE AND CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L36471; AAB9174.1; -.
DR HSSP; P05082; 2ECK.
DR InterPro; IPR000850; Adenylate_kin.
DR Pfam; PF00406; adenylatekinase; 1.
DR PRINTS; PR00094; ADENYLKINASE.
DR ProDom; PD000657; Adenylate_kin; 1.
DR PROSITE; PS00113; ADENYLATE_KINASE; 1.

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KW Transferase; Kinase; ATP-binding.  
 FT NP\_BIND 7 15 ATP (BY SIMILARITY).  
 SQ SEQUENCE 215 AA; 23124 MW; 24629AA075539BED CRC64;

Query Match 83.9%; Score 26; DB 1; Length 215;  
 Best Local Similarity 71.4%; Pred. No. 52;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 piglxar 7  
 IIII I:  
 Db 44 PUGLEAK 50

Search completed: March 1, 2002, 06:52:07  
 Job time: 214 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2002, 06:48:13 ; Search time 22.94 Seconds  
(without alignments)  
44.634 Million cell updates/sec

Title: 09-876091-2  
Perfect score: 31  
Sequence: 1 p1glxar 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPTRMBL\_17:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_todent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	93.5	357	11 Q9D347	Q9D347 mus musculu
2	29	93.5	828	4 Q9HBX8	Q9HBX8 homo sapien
3	29	93.5	928	4 Q9BYD7	Q9BYD7 homo sapien
4	29	93.5	1201	1 Q9H070	Q9H070 mus musculu
5	28	90.3	122	11 Q9CQ87	Q9CQ87 mus musculu
6	28	90.3	130	10 Q6C448	Q6C448 arabidopsis
7	28	90.3	181	1 Q9UWPS	Q9UWPS pyrococcus
8	28	90.3	358	2 Q9ISJ3	Q9ISJ3 pseudomonas
9	28	90.3	363	2 Q9A361	Q9A361 caulobacter
10	28	90.3	367	2 Q9XB11	Q9XB11 mycobacteri
11	28	90.3	602	2 Q9F165	Q9F165 oryza sativ
12	27	87.1	169	10 Q9AWZ2	Q9AWZ2 oryza sativ
13	27	87.1	185	5 Q00837	Q00837 leishmania
14	27	87.1	189	12 Q9YMW9	Q9YMW9 lymantria d
15	27	87.1	216	2 Q9RL08	Q9RL08 streptomyce
16	27	87.1	228	11 Q9CCTA4	Q9CCTA4 mus musculu
17	27	87.1	373	2 Q9I140	Q9I140 pseudomonas
18	27	87.1	375	2 Q9A351	Q9A351 caulobacter
19	27	87.1	518	2 Q9RX13	Q9RX13 delinococcus

20	27	87.1	543	10 Q9SS50	Q9SS50 arabidopsis
21	27	87.1	551	2 Q9HYT4	Q9HYT4 pseudomonas
22	27	87.1	612	4 Q9P270	Q9P270 homo sapien
23	27	87.1	662	2 Q9PEB4	Q9PEB4 xyella fas
24	27	87.1	789	10 Q9CAR3	Q9CAR3 arabidopsis
25	27	87.1	1144	12 Q9QNC1	Q9QNC1 cucurbit gr
26	27	87.1	1648	12 Q9IR66	Q9IR66 cucurbit gr
27	27	87.1	1744	3 Q9A192	Q9A192 paracoccidi
28	26	83.9	89	5 Q9GM38	Q9GM38 leishmania
29	26	83.9	91	2 Q9JXX3	Q9JXX3 neisseria m
30	26	83.9	198	2 Q9PGM3	Q9PGM3 xyella fas
31	26	83.9	237	4 Q9S441	Q9S441 homo sapien
32	26	83.9	251	10 Q9FHT2	Q9FHT2 arabidopsis
33	26	83.9	259	2 Q52384	Q52384 pseudomonas
34	26	83.9	259	2 Q9L5D0	Q9L5D0 comamonas t
35	26	83.9	329	2 Q9RNE0	Q9RNE0 bacillus an
36	26	83.9	331	2 Q9KFR6	Q9KFR6 bacillus ha
37	26	83.9	358	2 Q9KCM5	Q9KCM5 bacillus ha
38	26	83.9	359	2 Q85469	Q85469 bacillus ce
39	26	83.9	361	2 Q99Z69	Q99Z69 streptococ
40	26	83.9	371	1 Q9HSF1	Q9HSF1 halobacteri
41	26	83.9	403	2 Q9Z552	Q9Z552 zymomonas m
42	26	83.9	440	2 Q9P661	Q9P661 mycobacteri
43	26	83.9	463	2 Q9EY75	Q9EY75 pseudomonas
44	26	83.9	473	2 Q51454	Q51454 pseudomonas
45	26	83.9	473	2 Q914N3	Q914N3 pseudomonas

## ALIGNMENTS

RESULT 1  
ID Q9D347 PRELIMINARY: PRT: 357 AA.  
AC Q9D347; 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE 9030405D14RIK PROTEIN.  
CN 9030405D14RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=COLON;  
RX MEDLINE=21085660; Pubmed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,  
RA Saito T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,  
RA Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kanuya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,  
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,  
RA Hayashizaki Y.;  
\*Functional annotation of a full-length mouse cDNA collection.\*;  
RT Nature 409:685-690(2001).  
RL EMBL: AK018485; BAB31233.1;  
MD: MGI:1918772; 9030405D14RIK.  
DR InterPro: IPR000101; Gamma-glutamyltranspeptidase.  
DR PRINTS: PR01210; GGTTRANSPTASE.  
SQ SEQUENCE 357 AA: 36875 MW: 2147725053675C1 CRC64;

Query Match  
Best Local Similarity 93.5%; Score 29; DB 11; Length 357;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 piglxar 7  
|||||  
DB 250 PGLGLAR 256

RESULT 2  
O9HBX8 PRELIMINARY; PRT; 828 AA.  
AC O9HBX8;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DE LEUCINE-RICH REPEAT-CONTAINING G PROTEIN-COUPLED RECEPTOR 6 (FRAGMENT).  
GN LGR6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hsu S.Y., Kudo M., Chen T., Nakabayashi K., van der Spek P.J., van Duin M., Hsueh A.J.W.;  
RT "The expanding family of leucine-rich repeat-containing G protein-coupled receptors (LGR): identification of LGR6 and LGR7 and the signaling mechanism for LGR7."  
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF190501; AAC17168.1; -  
DR InterPro: IPR000276; GPCR\_Rhodopsn.  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR003592; LRR\_out.  
DR InterPro: IPR003591; LRR\_typ.  
DR Pfam: PF00560; LRR; 10.  
DR PRINTS: PR00237; GPCR\_Rhodopsn.  
DR PRINTS: PR00019; LEURICHPT.  
DR SMART: SM00370; LRR; 5.  
DR SMART: SM00369; LRR\_Typ; 10.  
DR KIR Receptor.  
FT NON\_TER  
KW RECEPTOR  
SQ SEQUENCE 828 AA; 89387 MW; 12D9251EAA42D8B4 CRC64;

Query Match  
Best Local Similarity 93.5%; Score 29; DB 4; Length 828;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 piglxar 7  
|||||  
DB 372 PGLGLAR 378

RESULT 3  
O9BYD7 PRELIMINARY; PRT; 928 AA.  
AC O9BYD7;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DE VT520631 (FRAGMENT).  
GN VT520631.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Okazaki H., Hayashi A., Kozuma S., Salto T.;

RT "a member of g-protein coupled receptor family."  
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AB049405; BAB39854.1; -  
FT NON\_TER  
SQ SEQUENCE 928 AA; 100487 MW; 4C3364ADEA89C463 CRC64;

Query Match  
Best Local Similarity 93.5%; Score 29; DB 4; Length 928;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 piglxar 7  
|||||  
DB 472 PGLGLAR 478

RESULT 4  
O9HU70 PRELIMINARY; PRT; 1201 AA.  
AC O9HU70;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DE HYPOTHETICAL PROTEIN PA5114.  
GN PA5114.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OX NCBI\_TaxID=287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-PA01;  
RX MEDLINE=20437337; PubMed=10984043;  
RA Stover C.K., Phan X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P., Hickey M.J., Brinkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M., Gaderer L.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Labig K., Lam R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen."  
RL Nature 406:959-964(2000).  
DR EMBL: AE004924; AAC08499.1; -  
DR InterPro: IPR002106; AA\_tRNA\_ligase\_II.  
DR PROSITE: PS00339; AA\_tRNA\_LIGASE\_II.2; UNKNOWN\_1.  
KW Hypothetical protein; Complete proteome  
SQ SEQUENCE 1201 AA; 128317 MW; 174A753AC7285833 CRC64;

Query Match  
Best Local Similarity 93.5%; Score 29; DB 2; Length 1201;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 piglxar 7  
|||||  
DB 488 PGLGLAR 494

RESULT 5  
O9COB7 PRELIMINARY; PRT; 122 AA.  
AC O9COB7;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DE 493040J24RIK PROTEIN (231004B22RIK PROTEIN).  
GN 493040J24RIK OR 231004B22RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.



RC STRAIN=C57BL/6J; TISSUE=TESTIS, AND TONGUE;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
RA Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,  
RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,  
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
DR EMBL; AK015083; BAB29706.1; -  
DR EMBL; AK009135; BAB26096.1; -  
DR MGD; MGI:1921169; 4930404J24Rik.  
DR MGD; MGI:1923685; 2310004B22Rik.  
SO SEQUENCE 122 AA; 14224 MW; A2E020FD0EA35E9 CRC64;

Query Match 90.3%; Score 28; DB 11; Length 122;  
Best Local Similarity 71.4%; Pred. NO. 48;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 plgixar 7  
1:1111  
Db 89 PIGLTR 95

RESULT 6  
O65448 PRELIMINARY; PRT; 130 AA.  
AC O65448;  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
DE HYPOTHETICAL 15.5 KDA PROTEIN.  
GN PIN20.100 OR A1942200.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bevan M., Medler H., Wambutt R., Bancroft I., Mewes H.W., Mayer K.,  
RA Schueller C.;  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
[2]  
RP SEQUENCE FROM N.A.  
RA Wambutt R., Mewes H.W., Lemcke K., Mayer K.F.X.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
[3]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL022140; CAA18103.1; -  
DR EMBL; AL161556; CAB79155.1; -  
KM Hypothetical protein.  
SO SEQUENCE 130 AA; 15455 MW; 544A52738B546667 CRC64;

Query Match 90.3%; Score 28; DB 10; Length 130;  
Best Local Similarity 71.4%; Pred. NO. 52;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 plgixar 7  
1:1111  
Db 46 PIGISAR 52

RESULT 7  
O9UWP5 PRELIMINARY; PRT; 181 AA.  
AC O9UWP5;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE OM HOMOLOG.  
OS Pyrococcus furiosus.  
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.  
OX NCBI\_TaxID=2261;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99445924; PubMed=10514376;  
RA Jenney F.E., Verhagen M.F.J.M., Cui X., Adams M.W.W.;  
RT "Anaerobic Microbes: Oxygen Detoxification Without Superoxide  
RT Dismutase.";  
RL Science 286:306-309(1999).  
DR EMBL; AF156097; AAF03230.1; -  
DR InterPro: IPR001197; Ribosomal\_L10E.  
DR Pfam: PF00826; Ribosomal\_L10e; 1  
SO SEQUENCE 181 AA; 20935 MW; 0A135A2D757727B0 CRC64;

Query Match 90.3%; Score 28; DB 1; Length 181;  
Best Local Similarity 71.4%; Pred. NO. 73;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 plgixar 7  
1:1111  
Db 119 PIGLAR 125

RESULT 8  
Q915J3 PRELIMINARY; PRT; 358 AA.  
AC Q915J3;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE HYPOTHETICAL PROTEIN PA0736.  
GN PA0736.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Pseudomonas.  
OX NCBI\_TaxID=287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PA01;  
RX MEDLINE=20437337; PubMed=10984043;  
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
RA Hickey M.J., Brinkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,  
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
RT opportunistic pathogen.";  
RL Nature 406:959-964(2000).  
DR EMBL; AE004508; AAG04125.1; -  
KM Hypothetical protein: Complete proteome.  
SO SEQUENCE 358 AA; 40019 MW; 035673AB6EDDA58 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 358;  
Best Local Similarity 71.4%; Pred. NO. 1.5e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 p1g1xar 7  
111:11

Db 349 P1G1AAR 355

## RESULT 9

09A361

PRELIMINARY; PRT; 363 AA.

AC 09A361; 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

GN GYCOOSYL TRANSFERASE, GROUP 1 FAMILY PROTEIN.

OC CC3345.

OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;

OC Caulobacter.

OX NCBI\_TaxID=69394;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21173698; PubMed=11259647;

RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

RA Deboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

RA Kolonel J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

RA Uterback S.L., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

RT "Complete genome sequence of Caulobacter crescentus.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

DR EMBL: AE005996; AAK25307.1; -

DR TIGR: CC3345; -

KM Transferase; Complete proteome.

SQ SEQUENCE 363 AA; 40710 MW; 2331A416BF7EED31 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 363;  
Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 p1g1xar 7  
111:11

Db 83 P1G1AAR 89

## RESULT 10

09XB11

PRELIMINARY; PRT; 367 AA.

AC 09XB11; 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

GN HYPOTHETICAL 39.4 KDA PROTEIN.

OS RVD2-ORF3 OR RVD2-ORF2.

OS Mycobacterium bovis BCG, and

OS Mycobacterium tuberculosis

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.

OX NCBI\_TaxID=33892; 1773;

RN [1]

RP SEQUENCE FROM N.A.

RX SPECIES=M. bovis BCG; STRAIN=BCG-PASTEUR;

RA MEDLINE=99255698; PubMed=10320585;

RA Gordon S.V., Brosch R., Billault A., Garnier T., Eiglmeier K.,

RA Cole S.T.;

RT "Identification of variable regions in the genomes of tubercle bacilli

RT using bacterial artificial chromosome arrays.";

RL Mol. Microbiol. 32:643-655(1999).

RN [2]

RN SEQUENCE FROM N.A.

RC SPECIES=M. tuberculosis; STRAIN=H37Ra;

RX MEDLINE=20002553; PubMed=10531227;  
RA Brosch R., Philipp W., Stavropoulos E., Colston M.J., Cole S.T.,  
RA Gordon S.V.,  
RT "Genomic analysis reveals variation between Mycobacterium tuberculosis  
RT H37Rv and the attenuated M. tuberculosis H37Ra.";  
RL Infect. Immun. 67:5768-5774(1999).  
DR EMBL: Y18606; CAB44658.1; -  
DR EMBL: AJ242907; CAB60071.1; -  
DR HSSP: P07850; ISOX.  
DR InterPro: IPR000572; Euk\_oxidored\_mol.yb.  
DR Pfam: PF00174; oxidored\_mol.yb; 1.  
DR PRINTS: PR00407; EUMOPTERIN.  
DR PROSITE: PS00559; MOLYBDOPTERIN\_EUK; UNKNOWN\_1.  
KM Hypothetical protein.  
SQ SEQUENCE 367 AA; 39410 MW; 3A0D3C024E864D20 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 367;  
Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 p1g1xar 7  
111:11

Db 326 P1G1TAR 332

## RESULT 11

09F165

PRELIMINARY; PRT; 602 AA.

AC 09F165; 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

GN METHYLMALONYL-COA MUTASE SMALL SUBUNIT (EC 5.4.99.2).

DE MCMA.

OS Amycolatopsis mediterranei.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Pseudonocardiaceae; Pseudonocardiaceae; Amycolatopsis.

OX NCBI\_TaxID=33910;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=U-32;

RA Zhang W.W., Yang L., Jiang W.H., Chiao J.S., Zhao G.P.;

RT "Cloning, sequencing and expression of the gene encoding

RT methylmalonyl-CoA mutase from Amycolatopsis mediterranei.";

RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL: AF117980; AAG47627.1; -

DR InterPro: IPR001629; MM\_COA\_mutase.

DR Pfam: PF01642; MM\_COA\_mutase; 1.

KM Isomerase.

SQ SEQUENCE 602 AA; 62668 MW; D396F2D3D76353A7 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 602;  
Best Local Similarity 71.4%; Pred. No. 2.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 p1g1xar 7  
111:11

Db 180 P1G1AAR 186

## RESULT 12

09AW22

PRELIMINARY; PRT; 169 AA.

AC 09AW22; 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

GN P0492F05.20 PROTEIN.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

OC Spermatothya; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponebare(GA3) genomic DNA, chromosome 1, PAC
  clone: P0492F05."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF002902; BAB32718.1; -;
SQ SEQUENCE 169 AA; 19010 MW; A4DA08F173FA5CCD CRC64;

Query Match
Best Local Similarity 87.1%; Score 27; DB 10; Length 169;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 plglxar 7
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Db 118 PLGLVAR 124

RESULT 13
O00837 PRELIMINARY; PRT; 185 AA.
AC O00837;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE GENE53.
GN GENE53.
OS Leishmania braziliensis.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5660;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MHOM/BR/75/M2903;
RX MEDLINE=98248915; Pubmed=9573393;
RA Fu G., Melville S., Brewster S., Warner J., Barker D.C.;
RT "Analysis of the genomic organisation of a small chromosome of
  Leishmania braziliensis M2903 reveals two genes encoding GTP-binding
  proteins, one of which belongs to a new G-protein family and is an
  RT antigen."
RL Gene 210:325-333(1998).
DR EMBL: U94966; AAC48330.1; -;
SQ SEQUENCE 185 AA; 20374 MW; 4AB3ACD679369AE4 CRC64;

Query Match
Best Local Similarity 87.1%; Score 27; DB 5; Length 185;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 plglxar 7
   ||| |
Db 52 PLGLAAR 58

RESULT 14
O9YMW9 PRELIMINARY; PRT; 189 AA.
AC O9YMW9;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE IDORF-5 PEPTIDE.
OS Lymantria dispar multicaud nuclear polyhedrosis virus (LDMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10449;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99124785; Pubmed=9887315;

```

```

RA Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,
RA Slavicek J.M., Rohmann G.F.;
RT "Sequence and analysis of the genome of a baculovirus pathogenic for
  RT Lymantria dispar."
RL Virology 253:17-34(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,
RA Slavicek J., Rohmann G.F.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Kuzio J.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF081810; AAC70190.1; -;
SQ SEQUENCE 189 AA; 21763 MW; 0048499C54C2EDB CRC64;

Query Match
Best Local Similarity 87.1%; Score 27; DB 12; Length 189;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 plglxar 7
   ||| |
Db 179 PLGLIAR 185

RESULT 15
O9RL08 PRELIMINARY; PRT; 216 AA.
AC O9RL08;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PUTATIVE TETR-FAMILY TRANSCRIPTIONAL REGULATOR.
GN SC569.19C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; Pubmed=8843436;
RA Redenbach M., Krieser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmid and a detailed genetic and physical map for
  the 8 Mb Streptomyces coelicolor A3(2) chromosome."
RL Mol. Microbiol. 21:77-96(1996).
CC -1- SIMILARITY: TO THE TETR/ACRR FAMILY OF TRANSCRIPTIONAL REGULATORS.
DR EMBL: AL117385; CAB55667.1; -;
DR InterPro: IPR001647; HTH_Tetr.
DR Pfam: PF00440; tetr.1.
DR PRINTS: PR00455; HTHTETR.
KW DNA-binding; Transcription regulation.
SQ SEQUENCE 216 AA; 24237 MW; 9C8EB6BC5C82270 CRC64;

Query Match
Best Local Similarity 87.1%; Score 27; DB 2; Length 216;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 plglxar 7

```

|||: ||  
Db 147 PLGIVAR 153

Search completed: March 1, 2002, 06:51:51  
Job time: 218 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2002, 06:47:48 ; Search time 23.88 Seconds  
(without alignments)  
21.713 Million cell updates/sec

Title: 09-876091-2  
Perfect score: 31  
Sequence: 1 plglxar 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

1: /SIDSB/gcgdata/geneseq/geneseq/AA1980.DAT:\*  
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4: /SIDSB/gcgdata/geneseq/geneseq/AA1983.DAT:\*  
5: /SIDSB/gcgdata/geneseq/geneseq/AA1984.DAT:\*  
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22: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	96.8	250	22	AA879216
2	30	96.8	259	22	AA869850
3	29	93.5	7	18	AAW24982
4	29	93.5	7	19	AAW51620
5	29	93.5	7	20	AAV90959
6	29	93.5	7	21	AA813515
7	29	93.5	7	21	AA814959
8	29	93.5	7	21	AA812590
9	29	93.5	7	21	AA855519
10	29	93.5	7	22	AA655039
11	29	93.5	7	22	AA897514

12	29	93.5	7	22	AA874962
13	29	93.5	7	22	AA872894
14	29	93.5	7	22	AA862797
15	29	93.5	7	22	AA850857
16	29	93.5	7	22	AA850351
17	29	93.5	8	19	AAW52141
18	29	93.5	8	20	AA869344
19	29	93.5	8	22	AA897518
20	29	93.5	9	19	AAW52136
21	29	93.5	10	22	AA897519
22	29	93.5	12	22	AA897521
23	29	93.5	497	20	AAV53574
24	29	93.5	847	20	AAV53575
25	28	90.3	7	18	AAW24983
26	28	90.3	7	22	AA874039
27	28	90.3	90	21	AA820531
28	28	90.3	90	21	AA859092
29	28	90.3	115	21	AA859576
30	28	90.3	130	21	AA820530
31	28	90.3	130	21	AA859091
32	28	90.3	155	21	AA859575
33	28	90.3	255	22	AA825925
34	28	90.3	1422	16	AA882069
35	28	90.3	1422	21	AA809039
36	27	87.1	262	22	AA892961
37	27	87.1	1143	22	AA831998
38	27	87.1	1144	22	AA831995
39	27	87.1	1644	22	AA832000
40	27	87.1	1645	22	AA831997
41	26	83.9	11	19	AAW73216
42	26	83.9	30	17	AA898936
43	26	83.9	82	21	AA828196
44	26	83.9	85	21	AAV44773
45	26	83.9	211	21	AA821686

#### ALIGNMENTS

RESULT 1  
ID AAB79216 standard; Protein; 250 AA.  
AC AAB79216;  
XX 30-APR-2001 (first entry)  
XX  
DE Corynebacterium glutamicum HA protein sequence SEQ ID NO:388.  
XX  
XX Corynebacterium glutamicum; homeostasis; adaptation; HA protein;  
KW fine chemical production; organic acid; proteinogenic amino acid;  
KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;  
KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;  
KW carboxylate; aromatic compound; vitamin; cofactor; polypeptide; enzyme;  
KW diagnosis; Corynebacterium diptheriae; genetic engineering;  
KW Brevibacterium; environmental condition.  
XX  
OS Corynebacterium glutamicum.  
XX  
XX WO200100842-A2.  
XX  
XX 04-JAN-2001.  
XX  
XX 23-JUN-2000; 2000WO-IB00911.  
XX  
XX 25-JUN-1999; 99US-0141031.  
PR 08-JUL-1999; 99DE-1031636.  
PR 09-JUL-1999; 99DE-1032125.  
PR 09-JUL-1999; 99DE-1032126.  
PR 09-JUL-1999; 99DE-1032127.  
PR 09-JUL-1999; 99DE-1032128.  
PR 09-JUL-1999; 99DE-1032129.  
PR 09-JUL-1999; 99DE-1032226.

Coumarin-labelled  
Human gelatinase i  
Peptide-Lipid conj  
Human gelatinase s  
Human gelatinase s  
Matrix metallopro  
Peptide SEQ ID NO:  
Substituted phosph  
Matrix metallopro  
Substituted phosph  
Human gonadotropin  
Human gonadotropin  
Recombinant human  
Synthetic collagen  
Arabidopsis thalia  
Arabidopsis thalia  
Arabidopsis thalia  
Arabidopsis thalia  
Human protein sequ  
Hepatitis GB virus  
Hepatitis GB virus  
C glutamicum prote  
Amino acid sequenc  
Amino acid sequenc  
Amino acid sequenc  
Amino acid sequenc  
MMP19 cleavage pep  
Synthetic human er  
Human artemisin neur  
Protein-1 compri  
Human mature eryth

PR 14-JUL-1999; 99DE-1032920.  
 PR 14-JUL-1999; 99DE-1032922.  
 PR 14-JUL-1999; 99DE-1032924.  
 PR 14-JUL-1999; 99DE-1032926.  
 PR 14-JUL-1999; 99DE-1032930.  
 PR 14-JUL-1999; 99DE-1032933.  
 PR 14-JUL-1999; 99DE-1032935.  
 PR 14-JUL-1999; 99DE-1032973.  
 PR 14-JUL-1999; 99DE-1033002.  
 PR 14-JUL-1999; 99DE-1033003.  
 PR 14-JUL-1999; 99DE-1033006.  
 PR 31-AUG-1999; 99DE-1041378.  
 PR 31-AUG-1999; 99DE-1041379.  
 PR 31-AUG-1999; 99DE-1041390.  
 PR 31-AUG-1999; 99DE-1041391.  
 PR 03-SEP-1999; 99DE-1042088.

XX (BADI ) BASF AG.

PI Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;

DR WPI: 2001-061974/07.

DR N-PSDB: AAF71331.

PT New isolated *Corynebacterium glutamicum* nucleic acid for production or  
 PT modulation of production of fine chemicals such as amino acids,  
 PT nucleosides, nucleotides, lipids, fatty acids, carbohydrates, vitamins  
 PT or enzymes -

XX Claim 20; Page 642-643; 712pp; English.

CC AAF71138 to AAF71357 encode the *Corynebacterium glutamicum* homeostasis  
 CC and adaptation (HA) proteins given in AAB79023 to AAB79242. The  
 CC C. glutamicum HA genes (1) can be used in vectors for expression in host  
 CC cells and production of fine chemicals, such as, an organic acid,  
 CC proteinogenic or nonproteinogenic amino acid (preferred), purine or  
 CC pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated  
 CC fatty acid, diol, carbohydrate, aromatic compound, vitamin, cofactor,  
 CC polypeptide or enzyme. The amino acids produced can be lysine, glutamine,  
 CC glutamate, alanine, aspartate, glycine, serine, threonine, methionine,  
 CC cysteine, valine, leucine, isoleucine, arginine, proline, histidine,  
 CC tyrosine, phenylalanine, or tryptophan. The fine chemical production can  
 CC be modulated. The presence of (1) or HA proteins encoded by then are  
 CC used for diagnosing the presence or activity of *Corynebacterium*  
 CC diphtheriae. (1) can be used to map the C. glutamicum genome or can be  
 CC used as markers for genetically engineered *Corynebacterium* or  
 CC *Brevibacterium*. The HA proteins encoded by the (1) are used to maintain  
 CC homeostasis in C. glutamicum or help the microorganism to adapt to  
 CC different environmental conditions.

XX Sequence 250 AA;

Query Match 96.8%; Score 30; DB 22; Length 250;

Best Local Similarity 85.7%; Pred. No. 19;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 plglxar 7

Db 236 plglxar 242

RESULT 2

ID AAG89850 standard; Protein: 259 AA.

XX AAG89850;

XX 26-SEP-2001 (first entry)

XX C-glutamicum protein fragment SEQ ID NO: 3604.

KM *Corynebacterium*; amino acid synthesis; vitamin; saccharide;

XX organic acid synthesis.

OS *Corynebacterium glutamicum*.

XX EPI108790-A2.

PD 20-JUN-2001.

PF 18-DEC-2000; 2000EP-0127688.

XX 16-DEC-1999; 99JP-0377484.

PR 07-APR-2000; 2000JP-0159162.

XX 03-AUG-2000; 2000JP-0280988.

XX (KYOW ) KYOWA HAKKO KOGYO KK.

PA Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

PI Tateishi N, Senoh A, Ikeda M, Ozaki A;

XX WPI: 2001-376931/40.

DR N-PSDB: AAH65069.

XX Novel polynucleotides derived from *Corynebacterium* bacteria, for identifying

PT mutation point of a gene, measuring expression of a gene, analysing

PT expression profile or pattern of a gene and identifying homologous gene

PT -

XX Claim 17; SEQ ID NO: 3604; 246pp + Sequence Listing; English.

XX The present invention provides a number of nucleotide and protein  
 CC sequences from the *Corynebacterium glutamicum* *Corynebacterium glutamicum*. These  
 CC are useful for identifying the mutation point of a gene derived from a  
 CC mutant of *Corynebacterium glutamicum*, measuring expression amount and  
 CC analysing the expression profile or expression pattern of a gene derived  
 CC from *Corynebacterium glutamicum*, and identifying a homologue of a gene derived  
 CC from *Corynebacterium glutamicum*. *Corynebacterium* bacteria are useful for producing  
 CC amino acids, nucleic acids, vitamins, saccharides and organic acids,  
 CC particularly L-lysine. The present sequence is a protein described  
 CC in the exemplification of the invention.

CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from the  
 CC European Patent Office.

XX Sequence 259 AA;

Query Match 96.8%; Score 30; DB 22; Length 259;  
 Best Local Similarity 85.7%; Pred. No. 20;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 plglxar 7

Db 245 plglxar 251

RESULT 3

ID AAW24982 standard; peptide: 7 AA.

XX AAW24982;

XX 03-DEC-1997 (first entry)

DE Recombinant human gelatinase fluorogenic peptide substrate #1.

XX Catalytic domain; human; gelatinase; matrix metalloproteinase; propeptide;

KM hemopeptin; fibronectin; vector; recombinant; deletion; hermia; joint;

XX vertebral disc; dermal ulcer; scar tissue.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1  
 FT /note= "Mca-Pro"  
 FT Modified-site 5  
 FT /label= "OTHER"  
 FT /note= "Dpa"  
 FT Modified-site 7  
 FT /note= "amidated C-terminus"  
 XX  
 PN US5646027-A.  
 XX  
 PD 08-JUL-1997.  
 XX  
 PF 08-SEP-1994; 94US-0303270.  
 XX  
 PR 08-SEP-1994; 94US-0303270.  
 XX  
 PA (WARN ) WARNER LAMBERT CO.  
 XX  
 PI Hupe DJ, Johnson LL, Ye Q;  
 XX  
 DR WPI; 1997-362935/33.  
 XX  
 PT Production of recombinant human gelatinase catalytic domain protein  
 PT - especially using vector containing new synthetic coding sequence  
 XX  
 PS Example 4; Column 11; 21pp; English.  
 XX  
 CC This peptide is a substrate for a novel recombinant catalytic domain of  
 CC the human 72 kD gelatinase, a member of the matrix metalloproteinase  
 CC family, lacking its propeptide, C-terminal hemopexin-like domain or  
 CC fibronectin-like insert (AAW24980). The catalytic domain protein is  
 CC useful for treating herniated vertebral discs, treating dermal ulcers,  
 CC modifying scar tissue formation and treating joint diseases.  
 XX  
 SQ Sequence 7 AA;

Query Match 93.5%; Score 29; DB 18; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 piglxar 7  
 |||||  
 Db 1 piglxar 7

RESULT 4  
 AAW51620  
 ID AAW51620 standard; peptide; 7 AA.  
 XX  
 AC AAW51620;  
 XX  
 DT 03-SEP-1998 (first entry)  
 XX  
 DE Peptide conjugated to lipid for use in liposomal drug delivery.  
 XX  
 KW Liposome; conjugate; drug delivery; peptidase-secreting cell;  
 KM tumour; diagnosis; therapy.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 5  
 FT /note= "Diphenylalanine"  
 FT Modified-site 7  
 FT /note= "C-terminal amide"  
 XX  
 PN W09816240-A1.  
 XX  
 PD 23-APR-1998.  
 XX  
 PF 15-OCT-1997; 97WO-US18538.  
 XX

PR 15-OCT-1996; 96US-0027544.  
 XX  
 PA (LIPO ) LIPOSOME CO INC.  
 XX  
 PI Ali S, Gabrallilly D, Erukulla RK, Franklin JC;  
 PI Janoff AS, Meers PR, Pak C;  
 DR WPI; 1998-261025/23.  
 XX  
 PT New peptide-lipid conjugates are incorporated into liposome(s) - to  
 PT selectively destabilise the liposome(s) in the vicinity of target  
 PT peptidase-secreting cells, e.g., tumour cells; useful in diagnosis  
 PT and therapy  
 XX  
 PS Claim 8; Page 33; 55pp; English.  
 XX  
 CC The invention relates to peptide-lipid conjugates and their use in  
 CC the preparation of liposomes which are predisposed to degradation in the  
 CC presence of peptidase-secreting cells and hence are targeted to these  
 CC cells. The liposomes can be used to treat mammalian diseases, disorders  
 CC and conditions, e.g. tumours, microbial infections and inflammation. The  
 CC liposomes allow selective delivery of an active agent to desired cells.  
 CC The liposomes are stable when the peptide remains conjugated to the  
 CC lipid. However, once the peptide portion of the conjugate is cleaved  
 CC from the lipid, by the action of cell-secreted peptidases, the liposomes  
 CC destabilise and release their contents in the vicinity of, or into, the  
 CC secreting cells. The liposomes can thus be used to treat conditions  
 CC characterised by the occurrence of peptidase-secreting cells. For  
 CC example, the breast cancer cell line MCF-7 is known to secrete elastase,  
 CC the levels of which are inversely correlated to overall survival in  
 CC breast cancer patients. The present sequence represents a specifically  
 CC claimed peptide which forms part of the peptide-lipid conjugate.  
 XX  
 SQ Sequence 7 AA;

Query Match 93.5%; Score 29; DB 19; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 piglxar 7  
 |||||  
 Db 1 piglxar 7

RESULT 5  
 AAY90959  
 ID AAY90959 standard; peptide; 7 AA.  
 XX  
 AC AAY90959;  
 XX  
 DT 31-AUG-2000 (first entry)  
 XX  
 DE Human matrix metalloproteinase 2 peptide.  
 XX  
 KW Human; matrix metalloproteinase 2; MMP-2; therapeutic; prophylactic;  
 KM glomerulopathy; collagenase IV; inhibitor; nephritis; diabetes.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "Pro is N-terminally modified to MOCAC-Pro"  
 FT Modified-site 5  
 FT /note= "X is A2Pr(Dnp)"  
 FT Modified-site 7  
 FT /note= "amidated"  
 XX  
 PN W09904780-A1.  
 XX  
 PD 04-FEB-1999.  
 XX  
 PF 17-JUL-1998; 98WO-JP03226.  
 XX

```

XX 22-JUL-1997; 97JP-0195414.
XX (SHIO ) SHIONOGI & CO LTD.
XX Kurihara H, Watanabe F, Tamura Y, Sinosaki T;
XX WPI: 1999-142583/12.
XX
XX Agent for treatment of glomerulopathy e.g. due to nephritis or diabetes
XX - comprises new or known sulphoramid compound
XX
XX Disclosure: Page 63; 102pp; Japanese.
XX
XX The present invention describes an agent for the treatment or prevention
XX of glomerulopathy. The agents of the present invention are collagenase IV
XX inhibitors and are useful for the treatment and prevention of
XX glomerulopathy (e.g. due to nephritis or diabetes). The present sequence
XX represents a human matrix metalloproteinase 2 (MMP-2) which is used in
XX the exemplification of the present invention.
XX
XX Sequence 7 AA:
SO
Query Match 93.5%; Score 29; DB 20; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 piglxar 7
1 | | | | |
Db 1 piglxar 7
RESULT 6
AAB13515
ID AAB13515 standard; peptide; 7 AA.
XX
XX AAB13515;
XX
XX 06-MAR-2001 (first entry)
XX
XX Human procollagen C-proteinase inhibition assay substrate #4.
DE
XX
XX Human; procollagen C-proteinase; PCP; bone morphogenetic protein-1;
XX BMP-1; collagen deposition; fibrotic disease; pericentral fibrosis;
XX interstitial pulmonary fibrosis; Symmers' fibrosis; kidney fibrosis;
XX perimuscular fibrosis; endocardial sclerosis; hepatitis; arthritis;
XX acute respiratory distress syndrome; cystic fibrosis; surgical adhesion;
XX scleroderma; restenosis.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1 /note= "modified by MCA"
XX Misc-difference 5 /note= "DPA"
XX Modified-site 7 /note= "C-terminal amide"
XX
XX WO200034313-A1.
XX
XX 15-JUN-2000.
XX
XX 06-DEC-1999; 99WO-EP09519.
XX
XX 10-DEC-1998; 98US-0111661.
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
XX
XX Dankwardt SM, Van Wart HE, Walker KAM;
XX
XX WPI: 2000-431271/37.

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XX New peptidic hydroxamic acid derivatives useful for treating fibrotic
XX diseases e.g. acute respiratory distress syndrome.
XX
XX Example 14; Page 62; 78pp; English.
XX
XX The present sequence is a peptide substrate which was used in an assay to
XX determine the efficiency of human procollagen C-proteinase (PCP, also
XX known as bone morphogenetic protein-1 or BMP-1) inhibitory compounds. PCP
XX is involved in the deposition of collagen. PCP inhibitors are useful as
XX they prevent excessive collagen deposition, and can be used to treat
XX fibrotic diseases such as interstitial pulmonary fibrosis, pericentral
XX fibrosis, Symmers' fibrosis, perimuscular fibrosis, kidney fibrosis,
XX endocardial sclerosis, hepatitis, acute respiratory distress syndrome,
XX arthritis, cystic fibrosis, surgical adhesions, tendon surgery, corneal
XX scarring, scleroderma, chronic allograft rejection, haemodialysis shunt
XX fibrosis and restenosis.
XX
XX Sequence 7 AA:
SO
Query Match 93.5%; Score 29; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 piglxar 7
1 | | | | |
Db 1 piglxar 7
RESULT 7
AAB14959
ID AAB14959 standard; peptide; 7 AA.
XX
XX AAB14959;
XX
XX 29-NOV-2000 (first entry)
XX
XX Fluorogenic substrate used to assay matrix metalloproteinases.
DE
XX
XX Matrix metalloproteinases; MMP; fluorescence; neoplasm;
XX atherosclerosis; inflammatory disease.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1 /note= "Fluorogenic N-terminal Mca"
XX Misc-difference 5 /note= "Given in specification as Dpa"
XX
XX WO200040564-A1.
XX
XX 13-JUL-2000.
XX
XX 30-NOV-1999; 99WO-US28339.
XX
XX 31-DEC-1998; 98US-0224549.
XX
XX (AVET ) AVENTIS PHARM INC.
XX
XX Warhowsky A, Janusz MJ, Flynn GA;
XX
XX WPI: 2000-465936/40.
XX
XX New benzazepine derivatives, useful for treatment of neoplastic states,
XX atherosclerosis and inflammatory diseases such as emphysema, chronic
XX bronchitis and asthma, are matrix metalloproteinase inhibitors.
XX
XX Example A; Page 64; 108pp; English.
XX
XX The present invention relates to benzolactam derivatives used as
XX inhibitors of matrix metalloproteinase. The benzolactam derivatives may

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CC be used for treatment of neoplastic states such as leukemias, carcinomas,  
 CC adenocarcinomas, sarcomas, melanomas and mixed neoplasias,  
 CC atherosclerosis, chronic inflammatory disease, rheumatoid arthritis,  
 CC osteoarthritis, cardiovascular disorders, corneal ulceration, dental  
 CC diseases and neurological disorders such as multiple sclerosis. The  
 CC present sequence is a fluorogenic substrate used to assay the activated  
 CC matrix metalloproteinases 1, 3 and 12. The matrix metalloproteinases  
 CC cleave the substrate at the Gly-Leu peptide bond, causing an increase  
 CC in fluorescence.

XX  
 SQ Sequence 7 AA:

Query Match 93.5%; Score 29; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 p1glxar 7  
 1111111  
 Db 1 p1glxar 7

RESULT 8

AA12590  
 ID AAB12590 standard; Peptide: 7 AA.

AC AAB12590;

DT 09-NOV-2000 (first entry)

DE Inhibition of collagenase activity assay substrate SEQ ID NO:8.

XX  
 KW Human; procollagen C-protein; PCP; bone morphogenetic protein 1; BMP-1;  
 KW sulphonamide hydroxamate; inhibitor; cytosolic; hepatotropic;  
 KW antiinflammatory; virucide; antiarthritic; vasotropic; vulnerary;  
 KW ophthalmological; interstitial collagen; interstitial pulmonary fibrosis;  
 KW Symmer's fibrosis; perimuscular fibrosis; kidney fibrosis; hepatitis;  
 KW liver fibrosis; idiopathic pulmonary fibrosis; endocardial sclerosis;  
 KW acute respiratory distress syndrome; arthritis; cystic fibrosis;  
 KW tendon surgery; surgical adhesion; corneal scarring; restenosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "Pro is N-terminally modified to MCA-Pro"

FT Modified-site 5 /note= "X is DPA, which is not defined further in

FT Modified-site 7 /note= "the specification"

FT WO200037436-A1.

XX PD 29-JUN-2000.

XX PF 14-DEC-1999; 99WO-EP09920.

XX PR 22-DEC-1998; 98US-0113311.

XX PR 03-AUG-1999; 99US-0147053.

XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX PI Billedeau RJ, Broke CA, Campbell JA, Chen JT, Dankwardt SM;

XX PI Delaet N, Robinson LA, Walker KAM;

XX DR WPI; 2000-514524/46.

XX PT New aryl sulphonamide hydroxamate derivatives useful for treatment of

XX PT e.g. fibrosis, arthritis and hepatitis, are procollagen C-proteinase

XX PT inhibitors -

XX PS Example 22; Page 109; 133pp; English.

XX The present invention describes aryl sulphonamide hydroxamate  
 CC derivatives. Aryl sulphonamide hydroxamate derivatives can be used for  
 CC the treatment of disease treatable by procollagen C-proteinase inhibitors  
 CC (especially interstitial collagen), e.g. interstitial pulmonary  
 CC fibrosis, Symmer's fibrosis, perimuscular fibrosis, kidney or liver  
 CC fibrosis, idiopathic pulmonary fibrosis, endocardial sclerosis,  
 CC hepatitis, acute respiratory distress syndrome, arthritis, cystic  
 CC fibrosis, tendon surgery, surgical adhesions, corneal scarring and  
 CC restenosis. They have cytosolic, hepatotropic, antiinflammatory,  
 CC virucide, antiarthritic, vasotropic, vulnerary and ophthalmological  
 CC activities. The present sequence represents a peptide substrate used in  
 CC an assay for the inhibition of collagenase activity, which is used in an  
 CC example from the present invention.

XX SQ Sequence 7 AA:

Query Match 93.5%; Score 29; DB 21; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 p1glxar 7  
 1111111  
 Db 1 p1glxar 7

RESULT 9

AAV85519  
 ID AAV85519 standard; peptide: 7 AA.

AC AAV85519;

DT 23-JUN-2000 (first entry)

DE Substrate for template-ligand conjugate.

XX Template ligand conjugate; triple helix coll; enzyme purification;  
 KW molecular modelling.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 5 /label= Dpa

FT Modified-site 7 /note= "hydroxyproline"

FT Modified-site 7 /note= "C-terminal amide"

FT WO200012538-A1.

XX PD 09-MAR-2000.

XX PF 23-AUG-1999; 99WO-US19367.

XX PR 31-AUG-1998; 98US-0144419.

XX PA (CHEN/) CHEN J.

XX PA (YEH/) YEH L.

XX PI Chen J, Yeh L;

XX DR WPI; 2000-246726/21.

XX PT New triple helix coil template having biologically active ligand,

XX PT useful for substrate based drug screening tool comprising increased

XX PT target specificity and affinity -

XX PS Example 2; Page 14; 29pp; English.

XX CC The invention relates to a template ligand conjugate (I) comprising a

XX CC template made of three cross linked polypeptide chains which each contain

XX CC tripeptide or hexapeptide repeat sequences aligned to form a triple helix



PI Karsdal M, Ovejero MDC, Schiodt CB, Winding B;  
 XX WPI: 2001-343189/36.  
 DR  
 XX  
 PT Use of new and known substituted phosphinate based peptide derivatives  
 PT for treating metabolic bone diseases e.g. osteoporosis or bone  
 PT metastasis -  
 PS  
 XX  
 PS Disclosure: Page 29; 149pp; English.  
 CC  
 CC The present invention describes the use of substituted phosphinate based  
 CC peptide derivatives for the treatment of metabolic bone diseases,  
 CC particularly those related to metalloproteinases. Bone diseases to be  
 CC treated include bone metastases (due to tumours) and osteoporosis. The  
 CC present sequence is a peptide described in the exemplification of the  
 CC invention.  
 CC  
 CC  
 SQ Sequence 7 AA;  
 Query Match 93.5%; Score 29; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 p1g1xar 7  
 |||||  
 Db 1 p1g1xar 7  
 RESULT 12  
 AAB74962  
 ID AAB74962 standard; Peptide: 7 AA.  
 XX  
 AC AAB74962;  
 XX  
 DT 11-JUL-2001 (first entry)  
 XX  
 DE Coumarin-labelled peptide matrix metalloproteinase substrate.  
 XX  
 KW Human; MMP: MMP1; collagenase 1; MMP2; gelatinase A; stromelysin;  
 KW arylsulfonylamido-substituted hydroxamic acid derivative; MMP inhibitor;  
 KW matrix degrading metalloproteinase; antiinflammatory; antirheumatic;  
 KW antiarthritic; osteopathic; cytostatic; hyperproliferative disease;  
 KW asthma; chronic obstructive pulmonary disease; COPD; tumour; metastasis;  
 KW inflammatory condition; rheumatoid arthritis; osteoarthritis;  
 KW pulmonary disease; emphysema.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT Modified-site /label= Pro is N-terminally labelled with MCA  
 FT Modified-site 5 /note= "given as Dpa in the specification"  
 FT Modified-site 7 /note= "amidated"  
 FT  
 XX  
 PN WO200110827-A1.  
 XX  
 PD 15-FEB-2001.  
 PD  
 PF 07-AUG-2000; 2000WO-EP07641.  
 PF  
 PR 09-AUG-1999; 99GB-0018684.  
 PR  
 XX (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GDS MBH.  
 XX  
 PI Breitenstein W, Hayakawa K, Iwasaki G, Kanazawa T, Kasacka T;  
 XX Koizumi S, Matsunaga S, Nakajima M, Sakaki J;  
 DR WPI: 2001-281265/29.  
 XX

PT New arylsulfonylamido-substituted hydroxamic acid derivatives, useful for  
 PT treating inflammatory conditions, rheumatoid arthritis, osteoarthritis,  
 PT tumors and pulmonary diseases, are matrix metalloproteinase inhibitors  
 PT -  
 PS  
 XX  
 PS Disclosure: Page 11; 98pp; English.  
 CC  
 CC The present invention describes arylsulfonylamido-substituted hydroxamic  
 CC acid derivatives (I). Also described are: (1) a pharmaceutical  
 CC composition comprising (I); and (2) preparation of (I). (I) has  
 CC antiinflammatory, antirheumatic, antiarthritic, osteopathic and  
 CC cytostatic activities, and can be used as an inhibitor of matrix  
 CC degrading metalloproteinase (MMP). (I) is useful for treating conditions  
 CC or diseases associated with MMP2 in warm blooded animals including  
 CC humans, such as hyperproliferative diseases, asthma, chronic obstructive  
 CC pulmonary disease (COPD) and tumours. (I) and pharmaceutical compositions  
 CC comprising (I) are useful in chemotherapy of tumours, COPD and asthma.  
 CC (I) is also useful for treating inflammatory conditions, rheumatoid  
 CC arthritis, osteoarthritis, tumours (tumour growth, metastasis,  
 CC progression or invasion), and pulmonary diseases (e.g. emphysema). The  
 CC present sequence represents a coumarin-labelled peptide matrix  
 CC metalloproteinase substrate, which is given in the exemplification of  
 CC the present invention.  
 CC  
 CC  
 SQ Sequence 7 AA;  
 Query Match 93.5%; Score 29; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 p1g1xar 7  
 |||||  
 Db 1 p1g1xar 7  
 RESULT 13  
 AAB72894  
 ID AAB72894 standard; peptide: 7 AA.  
 XX  
 AC AAB72894;  
 XX  
 DT 11-MAY-2001 (first entry)  
 XX  
 DE Human gelatinase inhibition assay substrate peptide.  
 XX  
 KW Metalloproteinase inhibitor; inflammation; cancer; autoimmune disease;  
 KW neurodegenerative disorder; cardiovascular disease; reprotolysin.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT Modified-site /label= OTHER  
 FT Modified-site 5 /note= "modified by MCA"  
 FT Modified-site /label= OTHER  
 FT Modified-site 7 /note= "Dpa"  
 FT Modified-site /label= OTHER  
 FT Modified-site 7 /note= "C-terminal amide"  
 FT  
 XX  
 PN WO200112611-A1.  
 XX  
 PD 22-FEB-2001.  
 PD  
 PF 03-AUG-2000; 2000WO-IB01090.  
 PF  
 PR 12-AUG-1999; 99US-0148547.  
 PR  
 PA (PFIZ ) PFIZER PROD INC.  
 XX  
 PI Blagg J;  
 XX



CC 3-(arylsulfonylamino)-tetrahydrofuran-3-carboxylic acid hydroxamide  
 CC compounds and their salts. These are useful for treating arthritis,  
 CC inflammatory bowel disease, Crohn's disease, emphysema, chronic  
 CC obstructive pulmonary disease, Alzheimer's disease, organ transplant  
 CC toxicity, cachexia, allergic reactions, allergic contact  
 CC hypersensitivity, cancer, tissue ulceration, restenosis, periodontal  
 CC disease, epidemolysis bullosa, osteoporosis, loosening of artificial  
 CC joint implants, atherosclerosis, aortic aneurysm, congestive heart  
 CC failure, myocardial infarction, stroke, cerebral ischaemia, head trauma,  
 CC spinal cord injury, neurodegenerative disorders, autoimmune disorders,  
 CC Huntington's disease, Parkinson's disease, migraine, depression,  
 CC peripheral neuropathy, pain, cerebral amyloid angiopathy, nootropic or  
 CC cognition enhancement, amyotrophic lateral sclerosis, multiple sclerosis,  
 CC ocular angiogenesis, corneal injury, macular degeneration, abnormal wound  
 CC healing, burns, diabetes, tumour invasion, tumour growth, tumour  
 CC metastasis, corneal scarring, scleritis, AIDS, sepsis and septic shock  
 in a mammal.  
 CC  
 XX  
 SQ Sequence 7 AA;

Query Match 93.5%; Score 29; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 plgixar 7  
 |||||  
 Db 1 plgixar 7

Search completed: March 1, 2002, 06:49:00  
 Job time: 72 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: March 1, 2002, 06:47:48 ; Search time 93.57 Seconds  
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Title: 09-876091-2  
Perfect score: 31  
Sequence: 1 plglxar 7

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Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/pdata/2/paa/US07\_COMB.pep: \*  
4: /cgn2\_6/pdata/2/paa/US08\_COMB.pep: \*  
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7: /cgn2\_6/pdata/2/paa/US083\_COMB.pep: \*  
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9: /cgn2\_6/pdata/2/paa/US085\_COMB.pep: \*  
10: /cgn2\_6/pdata/2/paa/US086\_COMB.pep: \*  
11: /cgn2\_6/pdata/2/paa/US087\_COMB.pep: \*  
12: /cgn2\_6/pdata/2/paa/US088\_COMB.pep: \*  
13: /cgn2\_6/pdata/2/paa/US089\_COMB.pep: \*  
14: /cgn2\_6/pdata/2/paa/US090\_COMB.pep: \*  
15: /cgn2\_6/pdata/2/paa/US091\_COMB.pep: \*  
16: /cgn2\_6/pdata/2/paa/US092\_COMB.pep: \*  
17: /cgn2\_6/pdata/2/paa/US093\_COMB.pep: \*  
18: /cgn2\_6/pdata/2/paa/US094\_COMB.pep: \*  
19: /cgn2\_6/pdata/2/paa/US095\_COMB.pep: \*  
20: /cgn2\_6/pdata/2/paa/US096\_COMB.pep: \*  
21: /cgn2\_6/pdata/2/paa/US097\_COMB.pep: \*  
22: /cgn2\_6/pdata/2/paa/US098\_COMB.pep: \*  
23: /cgn2\_6/pdata/2/paa/US099\_COMB.pep: \*  
24: /cgn2\_6/pdata/2/paa/US060\_COMB.pep: \*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	96.8	7	21	US-09-753-078-18
2	30	96.8	216	23	US-09-902-540-12039
3	30	96.8	226	16	US-09-252-991A-24343
4	30	96.8	259	21	US-09-738-626-3604
5	29	93.5	7	15	US-09-168-010-14
6	29	93.5	7	16	US-09-248-158-1
7	29	93.5	7	17	US-09-343-650-14
8	29	93.5	7	18	US-09-464-908A-1
9	29	93.5	7	21	US-09-753-078-8

10	29	93.5	7	22	US-09-808-832-209	Sequence 209, App
11	29	93.5	8	5	US-08-187-641A-3	Sequence 3, Appl
12	29	93.5	8	15	US-09-144-419-3	Sequence 3, Appl
13	29	93.5	78	21	US-09-758-456-212	Sequence 212, App
14	29	93.5	148	24	US-60-196-711-1240	Sequence 1240, App
15	29	93.5	133	21	US-09-758-468-421	Sequence 421, App
16	29	93.5	239	23	US-09-902-540-15424	Sequence 15424, A
17	29	93.5	259	23	US-09-902-540-12068	Sequence 12068, A
18	29	93.5	284	18	US-09-417-507-33272	Sequence 33272, A
19	29	93.5	333	19	US-09-562-737-7	Sequence 7, Appl
20	29	93.5	382	1	PCT-US01-08631-37569	Sequence 37569, A
21	29	93.5	497	16	US-09-243-991B-8	Sequence 8, Appl
22	29	93.5	559	24	US-60-212-655-421	Sequence 421, App
23	29	93.5	633	19	US-09-566-588A-5	Sequence 5, Appl
24	29	93.5	691	1	PCT-US01-08631-39673	Sequence 39673, A
25	29	93.5	734	16	US-09-252-991A-33036	Sequence 33036, A
26	29	93.5	736	19	US-09-566-588A-8	Sequence 8, Appl
27	29	93.5	847	16	US-09-243-991B-10	Sequence 10, Appl
28	29	93.5	937	24	US-60-229-515-1233	Sequence 1233, Ap
29	29	93.5	1275	1	PCT-US01-08631-36524	Sequence 36524, A
30	28	90.3	7	21	US-09-753-078-7	Sequence 7, Appl
31	28	90.3	7	21	US-09-753-078-16	Sequence 16, Appl
32	28	90.3	23	24	US-60-164-762-690	Sequence 690, App
33	28	90.3	23	24	US-60-169-840-7917	Sequence 7917, Ap
34	28	90.3	23	24	US-60-181-996-1261	Sequence 1261, Ap
35	28	90.3	90	20	US-09-617-681A-5238	Sequence 5238, Ap
36	28	90.3	255	1	PCT-US00-35017A-1440	Sequence 1440, Ap
37	28	90.3	383	16	US-09-252-991A-29457	Sequence 29457, A
38	28	90.3	649	24	US-60-215-652-5	Sequence 5, Appl
39	28	90.3	1422	6	US-08-242-654A-110	Sequence 110, Appl
40	28	90.3	1422	8	US-08-424-550A-84	Sequence 84, Appl
41	28	90.3	1422	8	US-08-424-550B-84	Sequence 84, Appl
42	28	90.3	1422	8	US-08-467-344A-84	Sequence 84, Appl
43	28	90.3	1422	8	US-08-469-260-84	Sequence 84, Appl
44	28	90.3	1422	8	US-08-469-260A-84	Sequence 84, Appl
45	28	90.3	1422	8	US-08-486-749-84	Sequence 84, Appl

#### ALIGNMENTS

RESULT 1  
US-09-753-078-18  
; Sequence 18, Application US/09753078  
; GENERAL INFORMATION:  
; APPLICANT: Mcgrath, Stephen  
; TITLE OF INVENTION: Use of Matrix Metalloproteinase Peptide Substrates to Lower  
; FILE REFERENCE: 11301-0210/44039-227523  
; CURRENT APPLICATION NUMBER: US/09/753.078  
; CURRENT FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 18  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Synthetic Peptide  
US-09-753-078-18

Query Match 96.8%; Score 30; DB 21; Length 7;  
Best Local Similarity 85.7%; Prod. No. 2.9e+06;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglxar 7  
|||  
Db 1 PLGLAAR 7

RESULT 2  
US-09-902-540-12039  
; Sequence 12039, Application US/09902540

GENERAL INFORMATION:  
APPLICANT: Goldman, Barry S.  
APPLICANT: Hinkle, Gregory J.  
APPLICANT: Slater, Steven C.  
APPLICANT: Miegand, Roger C.  
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
FILE REFERENCE: 38-10(15849)B  
CURRENT APPLICATION NUMBER: US/09/902,540  
CURRENT FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: 60/217,883  
PRIOR FILING DATE: 2000-07-10  
NUMBER OF SEQ ID NOS: 16825  
SEQ ID NO 12039  
LENGTH: 216  
TYPE: PRT  
ORGANISM: Myxococcus xanthus  
US-09-902-540-12039

Query Match 96.8%; Score 30; DB 23; Length 216;  
Best Local Similarity 85.7%; Pred. No. 2.6e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 plglxar 7  
|||||  
DB 191 PLGLSAR 197

RESULT 3  
US-09-252-991A-24343  
Sequence 24343, Application US/09252991A  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 24343  
LENGTH: 226  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-24343

Query Match 96.8%; Score 30; DB 16; Length 226;  
Best Local Similarity 85.7%; Pred. No. 2.8e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 plglxar 7  
|||||  
DB 33 PLGLAAR 39

RESULT 4  
US-09-738-626-3604  
Sequence 3604, Application US/09738626  
GENERAL INFORMATION:  
APPLICANT: NAKAGAWA, SATOSHI  
APPLICANT: MIZOGUCHI, HIROSHI  
APPLICANT: ANDO, SEIKO  
APPLICANT: HAYASHI, MIKIRO  
APPLICANT: OCHIAI, KEIKO  
APPLICANT: YOKOI, HARUKO  
APPLICANT: TATEISHI, NAOKO  
APPLICANT: SENOH, AKIHIRO  
APPLICANT: IKEDA, MASATO  
APPLICANT: OZAKI, AKIO

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-125  
CURRENT APPLICATION NUMBER: US/09/738,626  
CURRENT FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: JP 99/377484  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: JP 00/159162  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: JP 00/280988  
PRIOR FILING DATE: 2000-08-03  
NUMBER OF SEQ ID NOS: 7059  
SOFTWARE: PatentIn ver. 3.0  
SEQ ID NO 3604  
LENGTH: 259  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-09-738-626-3604

Query Match 96.8%; Score 30; DB 21; Length 259;  
Best Local Similarity 85.7%; Pred. No. 3.2e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 plglxar 7  
|||||  
DB 245 PLGLAAR 251

RESULT 5  
US-09-168-010-14  
Sequence 14, Application US/09168010  
GENERAL INFORMATION:  
APPLICANT: The Liposome Company Inc.  
APPLICANT: Pak, Charles  
APPLICANT: Meerts, Paul  
APPLICANT: Ali, Shaukat  
APPLICANT: Janoff, Andrew S.  
APPLICANT: Franklin, J. Craig  
APPLICANT: Erukulla, Ravi K.  
APPLICANT: Cabral-Lilly, Donna  
TITLE OF INVENTION: Liposomal peptide-lipid conjugates and  
TITLE OF INVENTION: Delivery Using Same  
FILE REFERENCE: TLC 215B  
CURRENT APPLICATION NUMBER: US/09/168,010  
CURRENT FILING DATE: 1998-10-08  
EARLIER APPLICATION NUMBER: US 60/027,544  
EARLIER FILING DATE: 1996-10-15  
NUMBER OF SEQ ID NOS: 44  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 14  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Peptides  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (5)...(5)  
OTHER INFORMATION: N-3-(2,4-dinitrophenyl)-L-2,3-diaminopropionyl  
NAME/KEY: BINDING  
LOCATION: (7)...(7)  
OTHER INFORMATION: C-terminal amino group  
US-09-168-010-14

Query Match 93.5%; Score 29; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.9e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 plglxar 7  
|||||  
DB 1 PLGLXAR 7



RESULT 6  
US-09-248-158-1  
: Sequence 1, Application US/09248158  
: GENERAL INFORMATION:  
: APPLICANT: Yuan, Zhengyu  
: APPLICANT: Chen, Zhong-Xiao  
: TITLE OF INVENTION: Direct Adsorption Scintillation Assay  
: TITLE OF INVENTION: for Measuring Enzyme Activity and Assaying Biochemical  
: FILE REFERENCE: 342312000600  
: CURRENT APPLICATION NUMBER: US/09/248,158  
: CURRENT FILING DATE: 1999-02-09  
: PRIOR APPLICATION NUMBER: 60/074,272  
: PRIOR FILING DATE: 1998-02-10  
: NUMBER OF SEQ ID NOS: 4  
: SOFTWARE: FastSeq for Windows Version 4.0  
: SEQ ID NO 1  
: LENGTH: 7  
: TYPE: PRT  
: ORGANISM: Unknown  
: FEATURE:  
: OTHER INFORMATION: Synthetic peptide  
: NAME/KEY: MOD\_RES  
: LOCATION: (2)...(2)  
: OTHER INFORMATION: 3H attached to Leucine  
US-09-248-158-1

Query Match 93.5%; Score 29; DB 16; Length 7;  
Best Local Similarity 85.7%; Pred. No. 2.9e+06;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 p1glxar 7  
111111  
DB 1 PGLIXAR 7

RESULT 7  
US-09-343-650-14  
: Sequence 1A, Application US/09343650  
: GENERAL INFORMATION:  
: APPLICANT: The Liposome Company Inc.  
: APPLICANT: Meers, Paul  
: APPLICANT: Pak, Charles  
: APPLICANT: Ali, Shaikat  
: APPLICANT: Janoff, Andrew S.  
: APPLICANT: Franklin, J. Craig  
: APPLICANT: Erukulla, Ravi K.  
: APPLICANT: Cabral-Lilly, Donna  
: TITLE OF INVENTION: Peptide-Lipid Conjugates, Liposomes and  
: FILE REFERENCE: T1C 213c  
: CURRENT APPLICATION NUMBER: US/09/343,650  
: CURRENT FILING DATE: 1999-06-29  
: EARLIER APPLICATION NUMBER: US 08/950,618  
: EARLIER FILING DATE: 1997-10-15  
: NUMBER OF SEQ ID NOS: 44  
: SOFTWARE: FastSeq for Windows Version 3.0  
: SEQ ID NO 14  
: LENGTH: 7  
: TYPE: PRT  
: ORGANISM: Peptides  
: FEATURE:  
: NAME/KEY: VARIANT  
: LOCATION: (5)...(5)  
: OTHER INFORMATION: N-3-(2,4-dinitrophenyl)-L-2,3-diaminopropionyl  
: FEATURE:  
: NAME/KEY: BINDING  
: LOCATION: (7)...(7)  
: OTHER INFORMATION: C-terminal amino group  
US-09-343-650-14

Query Match 93.5%; Score 29; DB 17; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.9e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 p1glxar 7  
111111  
DB 1 PGLIXAR 7

RESULT 8  
US-09-464-908A-1  
: Sequence 1, Application US/09464908A  
: GENERAL INFORMATION:  
: APPLICANT: Aventis Pharmaceuticals, Inc.  
: APPLICANT: Marshawsky, Alan  
: APPLICANT: Janusz, Michael  
: TITLE OF INVENTION: Selective Inhibitors of MMP-12  
: FILE REFERENCE: HMR2026A US  
: CURRENT APPLICATION NUMBER: US/09/464,908A  
: CURRENT FILING DATE: 1999-12-17  
: PRIOR APPLICATION NUMBER: 60/155,223  
: PRIOR FILING DATE: 1998-12-31  
: NUMBER OF SEQ ID NOS: 1  
: SOFTWARE: PatentIn version 3.0  
: SEQ ID NO 1  
: LENGTH: 7  
: TYPE: PRT  
: ORGANISM: Artificial sequence  
: FEATURE:  
: OTHER INFORMATION: Synthetic Construct  
: NAME/KEY: MISC FEATURE  
: LOCATION: (5)...(5)  
: OTHER INFORMATION: Xaa at position 5 is N-3-(2,4-dinitrophenyl)-L-2,3-diaminoprop  
US-09-464-908A-1

Query Match 93.5%; Score 29; DB 18; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.9e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 p1glxar 7  
111111  
DB 1 PGLIXAR 7

RESULT 9  
US-09-753-078-8  
: Sequence 8, Application US/09753078  
: GENERAL INFORMATION:  
: APPLICANT: Quirk, Stephen  
: APPLICANT: McGrath, Kevin  
: TITLE OF INVENTION: Use of Matrix Metalloproteinase Peptide Substrates to Lower  
: FILE REFERENCE: 11301-0210/44039-227523  
: CURRENT APPLICATION NUMBER: US/09/753,078  
: CURRENT FILING DATE: 2000-12-29  
: NUMBER OF SEQ ID NOS: 20  
: SOFTWARE: PatentIn version 3.0  
: SEQ ID NO 8  
: LENGTH: 7  
: TYPE: PRT  
: ORGANISM: Synthetic Peptide  
US-09-753-078-8

Query Match 93.5%; Score 29; DB 21; Length 7;  
Best Local Similarity 85.7%; Pred. No. 2.9e+06;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 p1glxar 7  
111111  
DB 1 PGLIXAR 7

RESULT 10  
US-09-808-832-209  
Sequence 209, Application US/09808832  
GENERAL INFORMATION:  
APPLICANT: Dupont Pharmaceuticals Company  
TITLE OF INVENTION: Peptidase-cleavable, targeted antineoplastic drugs and their ther  
FILE REFERENCE: use  
FILE REFERENCE: PH-7134  
CURRENT APPLICATION NUMBER: US/09/808,832  
CURRENT FILING DATE: 2001-03-15  
PRIOR APPLICATION NUMBER: 60/189,387  
PRIOR FILING DATE: 2000-03-15  
NUMBER OF SEQ ID NOS: 210  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 209  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (5)..(5)  
OTHER INFORMATION: diphenylalanine  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(7)  
OTHER INFORMATION: The synthesis of this peptide may be performed on an ABI 433A pep  
OTHER INFORMATION: tide synthesizer using readily available materials well known to  
US-09-808-832-209

Query Match 93.5%; Score 29; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.9e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglxar 7  
Db 1 PLGLXAR 7

RESULT 11  
US-08-187-641A-3  
Sequence 3, Application US/08187641A  
GENERAL INFORMATION:  
APPLICANT: Chen, James M.  
TITLE OF INVENTION: TRIPLE HELIX COIL TEMPLATE HAVING A  
TITLE OF INVENTION: BIOLOGICALLY ACTIVE LIGAND  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millitia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02713  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/187,641A  
FILING DATE: 27-JAN-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: McNeill, Scott A.  
REGISTRATION NUMBER: 37,185  
REFERENCE/DOCKET NUMBER: OS193-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-187-641A-3

Query Match 93.5%; Score 29; DB 5; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.9e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglxar 7  
Db 2 PLGLXAR 8

RESULT 12  
US-09-144-419-3  
Sequence 3, Application US/09144419  
GENERAL INFORMATION:  
APPLICANT: Chen, James  
TITLE OF INVENTION: TRIPLE HELIX COIL TEMPLATE HAVING A BIOLOGICALLY ACTIVE LIGAND  
FILE REFERENCE: 08083/002001  
CURRENT APPLICATION NUMBER: US/09/144,419  
CURRENT FILING DATE: 1998-08-31  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (1)...(1)  
OTHER INFORMATION: Xaa = 7-methoxycomurain-4-yl  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (6)...(6)  
OTHER INFORMATION: Xaa = N-3(2,4-dinitrophenyl)-L-2,3-diaminopropionyl  
US-09-144-419-3

Query Match 93.5%; Score 29; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.9e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 plglxar 7  
Db 2 PLGLXAR 8

RESULT 13  
US-09-758-456-212  
Sequence 212, Application US/09758456  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PM021  
CURRENT APPLICATION NUMBER: US/09/758,456  
CURRENT FILING DATE: 2001-01-11  
PRIOR APPLICATION NUMBER: 60/179,065  
PRIOR FILING DATE: 2000-01-31  
PRIOR APPLICATION NUMBER: 60/180,628  
PRIOR FILING DATE: 2000-02-04  
NUMBER OF SEQ ID NOS: 384  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 212  
LENGTH: 78  
TYPE: PRT

```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (15)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (28)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-758-456-212

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```

Query Match          93.5%; Score 29; DB 21; Length 78;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Oy 1 plglxar 7
    |||||
Db 30 PLGLHAR 36

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RESULT 14
US-60-196-711-1240
; Sequence 1240, Application US/60196711
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS OF THE
; TITLE OF INVENTION: SER/THR AND TYR FAMILY OF KINASES, NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING THESE HUMAN KINASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: C1000452
; CURRENT APPLICATION NUMBER: US/60/196,711
; CURRENT FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 2378
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1240
; LENGTH: 148
; TYPE: PRT
; ORGANISM: HUMAN
US-60-196-711-1240

```

```

Query Match          93.5%; Score 29; DB 24; Length 148;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Oy 1 plglxar 7
    |||||
Db 119 PLGLHAR 125

```

```

RESULT 15
US-09-758-468-421
; Sequence 421, Application US/09758468
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM034
; CURRENT APPLICATION NUMBER: US/09/758,468
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 421
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (124)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE

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```

; LOCATION: (135)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (152)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (173)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (177)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (182)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (187)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-758-468-421

```

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Query Match          93.5%; Score 29; DB 21; Length 193;
Best Local Similarity 85.7%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

Oy 1 plglxar 7
    |||||
Db 25 PLGLEAR 31

```

```

Search completed: March 1, 2002, 06:50:40
Job time: 172 sec

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OM protein - protein search, using sw model

Run on: March 1, 2002, 06:47:52 ; Search time 32.98 Seconds  
(without alignments)  
9.535 Million cell updates/sec

Title: 09-876091-2  
Perfect score: 31  
Sequence: 1 pligixar 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 216105 seqs, 44922408 residues

Total number of hits satisfying chosen parameters: 216105

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_New:\*  
1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/ptodata/1/paa/US50\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES				Description	
Result No.	Score	Query Match Length	ID		
1	96.8	148	US-09-620-111B-7170	Sequence 7170, Ap	
2	93.5	424	US-10-015-127-10198	Sequence 10198, A	
3	93.5	794	US-09-844-362-7	Sequence 7, Appli	
4	93.5	823	US-09-844-362-6	Sequence 6, Appli	
5	93.5	828	US-09-844-362-2	Sequence 2, Appli	
6	93.5	915	US-09-844-362-5	Sequence 5, Appli	
7	93.5	967	US-09-988-922-48	Sequence 48, Appli	
8	93.5	977	US-09-988-922-68	Sequence 68, Appli	
9	90.3	90	US-09-620-394B-4083	Sequence 4083, Ap	
10	90.3	90	US-09-708-427-40203	Sequence 40203, A	
11	90.3	130	US-09-620-394B-4082	Sequence 4082, Ap	
12	90.3	130	US-09-708-427-40202	Sequence 40202, A	
13	90.3	134	US-09-708-427-60383	Sequence 60383, A	
14	90.3	137	US-09-708-427-84737	Sequence 84737, A	
15	90.3	171	US-09-708-427-60382	Sequence 60382, A	
16	90.3	496	US-10-015-127-12831	Sequence 12831, A	
17	90.3	649	US-09-611-526-3436	Sequence 3436, Ap	
18	90.3	756	US-10-015-127-11097	Sequence 11097, A	
19	87.1	138	US-09-620-394B-2	Sequence 2, Appli	
20	87.1	262	US-09-605-703B-872	Sequence 872, App	
21	87.1	262	US-09-605-703B-874	Sequence 874, App	
22	83.9	8	US-10-007-649-54	Sequence 49, Appli	
23	83.9	8	US-10-007-649-54	Sequence 54, Appli	
24	83.9	128	US-09-620-111B-5545	Sequence 5545, Ap	
25	83.9	532	US-09-966-614-2	Sequence 2, Appli	
26	80.6	37	US-10-029-386-34077	Sequence 34077, A	

27	25	80.6	53	5	US-09-620-111B-6728	Sequence 6728, Ap
28	25	80.6	84	5	US-09-828-792-842	Sequence 842, App
29	25	80.6	84	5	US-09-836-614-496	Sequence 496, App
30	25	80.6	112	5	US-09-708-427-47189	Sequence 47189, A
31	25	80.6	130	6	US-10-015-127-13409	Sequence 13409, A
32	25	80.6	152	5	US-09-708-427-34517	Sequence 34517, A
33	25	80.6	190	5	US-09-708-427-30888	Sequence 30888, A
34	25	80.6	204	5	US-09-620-394B-4561	Sequence 4561, App
35	25	80.6	240	5	US-09-826-734-94	Sequence 94, Appli
36	25	80.6	240	5	US-09-826-734-94	Sequence 112, Appli
37	25	80.6	249	6	US-10-029-386-33807	Sequence 33807, A
38	25	80.6	250	5	US-09-397-945-180	Sequence 180, App
39	25	80.6	265	5	US-09-611-526-3915	Sequence 3915, App
40	25	80.6	275	5	US-09-620-394B-4560	Sequence 4560, App
41	25	80.6	283	5	US-09-397-945-333	Sequence 333, App
42	25	80.6	292	5	US-09-708-427-56647	Sequence 56647, A
43	25	80.6	307	5	US-09-708-427-56646	Sequence 56646, A
44	25	80.6	330	4	US-08-974-524E-345	Sequence 345, App
45	25	80.6	330	6	US-10-053-758-203	Sequence 203, App

## ALIGNMENTS

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RESULT 1
US-09-620-111B-7170
; Sequence 7170, Application US/09620111B
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide
; FILE REFERENCE: 2750-1070P
; CURRENT APPLICATION NUMBER: US/09/620,111B
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 9298
; SEQ ID NO 7170
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..148
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..148
; OTHER INFORMATION: Ceres Seq. ID 1339448
US-09-620-111B-7170

Query Match      96.8%; Score 30; DB 5; Length 148;
Best Local Similarity 85.7%; Pred. No. 4.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Ox 1 pligixar 7
    ||| |
Db 9 PLIGSAR 15

RESULT 2
US-10-015-127-10198
; Sequence 10198, Application US/10015127
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley G.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Spingomonas elodea genome sequences and uses thereof
; FILE REFERENCE: 38-10(15806)B
; CURRENT APPLICATION NUMBER: US/10/015,127
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/252,455
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 14357
; SEQ ID NO 10198
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LENGTH: 424  
TYPE: PRT  
ORGANISM: Spingomonas elodea  
US-10-015-127-10198

Query Match 93.5%; Score 29; DB 6; Length 424;  
Best Local Similarity 85.7%; Pred. No. 23;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 piglxar 7  
111111  
DB 10 PLGLLAR 16

RESULT 3  
US-09-844-362-7  
Sequence 7, Application US/09844362  
GENERAL INFORMATION:  
APPLICANT: ZHU, Shiaooping et al.  
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
FILE REFERENCE: CLO01146  
CURRENT APPLICATION NUMBER: US/09/844,362  
CURRENT FILING DATE: 2001-04-30  
PRIOR APPLICATION NUMBER: US 60/270,873  
PRIOR FILING DATE: 2001-02-26  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 794  
TYPE: PRT  
ORGANISM: Human  
US-09-844-362-7

Query Match 93.5%; Score 29; DB 5; Length 794;  
Best Local Similarity 85.7%; Pred. No. 46;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 piglxar 7  
111111  
DB 343 PLGLLAR 349

RESULT 4  
US-09-844-362-6  
Sequence 6, Application US/09844362  
GENERAL INFORMATION:  
APPLICANT: ZHU, Shiaooping et al.  
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
FILE REFERENCE: CLO01146  
CURRENT APPLICATION NUMBER: US/09/844,362  
CURRENT FILING DATE: 2001-04-30  
PRIOR APPLICATION NUMBER: US 60/270,873  
PRIOR FILING DATE: 2001-02-26  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 823  
TYPE: PRT  
ORGANISM: Human  
US-09-844-362-6

Query Match 93.5%; Score 29; DB 5; Length 823;  
Best Local Similarity 85.7%; Pred. No. 48;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 piglxar 7

DB 372 PLGLLAR 378  
111111

RESULT 5  
US-09-844-362-2  
Sequence 2, Application US/09844362  
GENERAL INFORMATION:  
APPLICANT: ZHU, Shiaooping et al.  
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
FILE REFERENCE: CLO01146  
CURRENT APPLICATION NUMBER: US/09/844,362  
CURRENT FILING DATE: 2001-04-30  
PRIOR APPLICATION NUMBER: US 60/270,873  
PRIOR FILING DATE: 2001-02-26  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 828  
TYPE: PRT  
ORGANISM: Human  
US-09-844-362-2

Query Match 93.5%; Score 29; DB 5; Length 828;  
Best Local Similarity 85.7%; Pred. No. 49;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 piglxar 7  
111111  
DB 372 PLGLLAR 378

RESULT 6  
US-09-844-362-5  
Sequence 5, Application US/09844362  
GENERAL INFORMATION:  
APPLICANT: ZHU, Shiaooping et al.  
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
FILE REFERENCE: CLO01146  
CURRENT APPLICATION NUMBER: US/09/844,362  
CURRENT FILING DATE: 2001-04-30  
PRIOR APPLICATION NUMBER: US 60/270,873  
PRIOR FILING DATE: 2001-02-26  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 915  
TYPE: PRT  
ORGANISM: Human  
US-09-844-362-5

Query Match 93.5%; Score 29; DB 5; Length 915;  
Best Local Similarity 85.7%; Pred. No. 54;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 piglxar 7  
111111  
DB 459 PLGLLAR 465

RESULT 7  
US-09-988-922-48  
Sequence 48, Application US/09988922  
GENERAL INFORMATION:  
APPLICANT: Erding Hu  
APPLICANT: Yuan Zhu  
APPLICANT: Ganesh M. Sathe

```

: APPLICANT: Joyce Yue Mao
: APPLICANT: Wendy S. Halsey
: APPLICANT: Jon Chambers
: APPLICANT: Allison Isobel Muir
: APPLICANT: Philip Graham Szekeres
: APPLICANT: Usman Shabon
: APPLICANT: Derek J. Bergsma
: APPLICANT: Nabil A. Elshourbagy
: APPLICANT: David Michalovich
: APPLICANT: Pamela A. Lane
: APPLICANT: Menelas N. Pangalos
: APPLICANT: Melanie Robbins
: APPLICANT: David Malcolm Duckworth
: APPLICANT: Jeffrey Hill
: APPLICANT: Ping Tsui
: APPLICANT: Pankaj Agarwal
: APPLICANT: Randall Forrest Smith
: APPLICANT: Lisa Vawter
: APPLICANT: Catherine E. Ellis
: APPLICANT: Manhandeeswar Gattu
: APPLICANT: John W. Quillen, Jr.
: APPLICANT: Erin M. Toland
: APPLICANT: Steven Michael Foord
: APPLICANT: Han Ngoc Trinh
: APPLICANT: Alexander Taylor
: APPLICANT: Henry Sarau
: APPLICANT: Steven Ruben
: APPLICANT: George H. Poste
: APPLICANT: Michel Louis Souchet
: APPLICANT: Philippe Laurent Robert
: APPLICANT: Stephane Clement Krief
: APPLICANT: Bernard Emile Joseph Gout
: APPLICANT: Eve Mahe
: TITLE OF INVENTION: HUMAN G PROTEIN-COUPLED RECEPTOR
: TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
: FILE REFERENCE: GP-70775B-C1
: CURRENT APPLICATION NUMBER: US/09/988,922
: CURRENT FILING DATE: 2001-11-19
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 48
: LENGTH: 967
: TYPE: PRT
: ORGANISM: HOMO SAPIENS
US-09-988-922-48

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Query Match      93.5%; Score 29; DB 5; Length 967;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Oy 1 plglxar 7
Db 511 PLGLLAR 517

```

```

RESULT 8
US-09-988-922-68
: Sequence 68, Application US/09988922
: GENERAL INFORMATION:
: APPLICANT: Erding Hu
: APPLICANT: Yuan Zhu
: APPLICANT: Ganesh M. Sathe
: APPLICANT: Joyce Yue Mao
: APPLICANT: Wendy S. Halsey
: APPLICANT: Jon Chambers
: APPLICANT: Allison Isobel Muir
: APPLICANT: Philip Graham Szekeres
: APPLICANT: Usman Shabon
: APPLICANT: Derek J. Bergsma
: APPLICANT: Nabil A. Elshourbagy
: APPLICANT: David Michalovich
: APPLICANT: Pamela A. Lane

```

```

: APPLICANT: Menelas N. Pangalos
: APPLICANT: Melanie Robbins
: APPLICANT: David Malcolm Duckworth
: APPLICANT: Jeffrey Hill
: APPLICANT: Ping Tsui
: APPLICANT: Pankaj Agarwal
: APPLICANT: Randall Forrest Smith
: APPLICANT: Lisa Vawter
: APPLICANT: Catherine E. Ellis
: APPLICANT: Manhandeeswar Gattu
: APPLICANT: John W. Quillen, Jr.
: APPLICANT: Erin M. Toland
: APPLICANT: Steven Michael Foord
: APPLICANT: Han Ngoc Trinh
: APPLICANT: Alexander Taylor
: APPLICANT: Steven Ruben
: APPLICANT: George H. Poste
: APPLICANT: Michel Louis Souchet
: APPLICANT: Philippe Laurent Robert
: APPLICANT: Stephane Clement Krief
: APPLICANT: Bernard Emile Joseph Gout
: APPLICANT: Eve Mahe
: TITLE OF INVENTION: HUMAN G PROTEIN-COUPLED RECEPTOR
: TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
: FILE REFERENCE: GP-70775B-C1
: CURRENT APPLICATION NUMBER: US/09/988,922
: CURRENT FILING DATE: 2001-11-19
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 68
: LENGTH: 977
: TYPE: PRT
: ORGANISM: HOMO SAPIENS
US-09-988-922-68

```

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Query Match      93.5%; Score 29; DB 5; Length 977;
Best Local Similarity 85.7%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Oy 1 plglxar 7
Db 521 PLGLLAR 527

```

```

RESULT 9
US-09-620-394B-4083
: Sequence 4083, Application US/09620394B
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nickolai
: APPLICANT: Brover, Vyacheslav
: TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptid
: FILE REFERENCE: 2750-1067P
: CURRENT APPLICATION NUMBER: US/09/620,394B
: CURRENT FILING DATE: 2000-07-21
: NUMBER OF SEQ ID NOS: 9131
: SEQ ID NO 4083
: LENGTH: 90
: TYPE: PRT
: ORGANISM: Arabidopsis thaliana
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 1..90
: OTHER INFORMATION: Xaa is any amino acid
: NAME/KEY: misc.feature
: LOCATION: 1..90
: OTHER INFORMATION: Ceres Seq. ID 1388505
US-09-620-394B-4083

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Query Match      90.3%; Score 28; DB 5; Length 90;

```

Best Local Similarity 71.4%; Pred. No. 7.7;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 plglxar 7  
|||: ||  
Db 6 PLGISAR 12

RESULT 10  
US-09-708-427-40203  
; Sequence 40203, Application US/09708427  
; GENERAL INFORMATION:  
; APPLICANT: N. ALEXANDROV et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1243P  
; CURRENT APPLICATION NUMBER: US/09/708,427  
; CURRENT FILING DATE: 2000-11-09  
; NUMBER OF SEQ ID NOS: 85364  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 40203  
; LENGTH: 90  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc-feature  
; LOCATION: 1..90  
; OTHER INFORMATION: Xaa is any amino acid  
; NAME/KEY: misc-feature  
; LOCATION: 1..90  
; OTHER INFORMATION: Ceres Seq. ID 1842638  
US-09-708-427-40203

Query Match 90.3%; Score 28; DB 5; Length 90;  
Best Local Similarity 71.4%; Pred. No. 7.7;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 plglxar 7  
|||: ||  
Db 6 PLGISAR 12

RESULT 11  
US-09-620-394B-4082  
; Sequence 4082, Application US/09620394B  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai  
; FILE REFERENCE: 2750-1243P  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1067P  
; CURRENT APPLICATION NUMBER: US/09/620,394B  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 9131  
; SEQ ID NO 4082  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc-feature  
; LOCATION: 1..130  
; OTHER INFORMATION: Xaa is any amino acid  
; NAME/KEY: misc-feature  
; LOCATION: 1..130  
; OTHER INFORMATION: Ceres Seq. ID 1388504  
US-09-620-394B-4082

Query Match 90.3%; Score 28; DB 5; Length 130;  
Best Local Similarity 71.4%; Pred. No. 11;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 plglxar 7  
|||: ||  
Db 46 PLGISAR 52

RESULT 12  
US-09-708-427-40202  
; Sequence 40202, Application US/09708427  
; GENERAL INFORMATION:  
; APPLICANT: N. ALEXANDROV et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID  
; FILE REFERENCE: 2750-1243P  
; CURRENT APPLICATION NUMBER: US/09/708,427  
; CURRENT FILING DATE: 2000-11-09  
; NUMBER OF SEQ ID NOS: 85364  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 40202  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: misc-feature  
; LOCATION: 1..130  
; OTHER INFORMATION: Xaa is any amino acid  
; NAME/KEY: misc-feature  
; LOCATION: 1..130  
; OTHER INFORMATION: Ceres Seq. ID 1842637  
US-09-708-427-40202

Query Match 90.3%; Score 28; DB 5; Length 130;  
Best Local Similarity 71.4%; Pred. No. 11;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 plglxar 7  
|||: ||  
Db 46 PLGISAR 52

RESULT 13  
US-09-708-427-60383  
; Sequence 60383, Application US/09708427  
; GENERAL INFORMATION:  
; APPLICANT: N. ALEXANDROV et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID  
; FILE REFERENCE: 2750-1243P  
; CURRENT APPLICATION NUMBER: US/09/708,427  
; CURRENT FILING DATE: 2000-11-09  
; NUMBER OF SEQ ID NOS: 85364  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 60383  
; LENGTH: 134  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc-feature  
; LOCATION: 1..134  
; OTHER INFORMATION: Xaa is any amino acid  
; NAME/KEY: misc-feature  
; LOCATION: 1..134  
; OTHER INFORMATION: Ceres Seq. ID 1947093  
US-09-708-427-60383

Query Match 90.3%; Score 28; DB 5; Length 134;  
Best Local Similarity 71.4%; Pred. No. 12;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 plglxar 7  
|||: ||  
Db 62 PLGISAR 68



Search completed: March 1, 2002, 06:51:20  
Job time: 208 sec

RESULT 14  
US-09-708-427-84737

: Sequence 84737, Application US/09708427

: GENERAL INFORMATION:

: APPLICANT: N. ALEXANDROV et al.

: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

: TITLE OF INVENTION: THEREBY

: FILE REFERENCE: 2750-1243P

: CURRENT APPLICATION NUMBER: US/09/708,427

: CURRENT FILING DATE: 2000-11-09

: NUMBER OF SEQ ID NOS: 85364

: SOFTWARE: PatentIn version 3.1

: SEQ ID NO 84737

: LENGTH: 137

: TYPE: PRT

: ORGANISM: Zea mays subsp. mays

: FEATURE:

: NAME/KEY: misc\_feature

: LOCATION: 1..137

: OTHER INFORMATION: Xaa is any amino acid

: NAME/KEY: misc\_feature

: LOCATION: 1..137

: OTHER INFORMATION: Ceres Seq. ID 1964815

: US-09-708-427-84737

: Query Match

: Best Local Similarity 90.3%; Score 28; DB 5; Length 137;

: Matches 5; Conservative 1; Mismatches 0; Gaps 0;

: QY 1 plglxar 7

: Db 55 PLGISAR 61

: RESULT 15

: US-09-708-427-60382

: Sequence 60382, Application US/09708427

: GENERAL INFORMATION:

: APPLICANT: N. ALEXANDROV et al.

: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

: TITLE OF INVENTION: THEREBY

: FILE REFERENCE: 2750-1243P

: CURRENT APPLICATION NUMBER: US/09/708,427

: CURRENT FILING DATE: 2000-11-09

: NUMBER OF SEQ ID NOS: 85364

: SOFTWARE: PatentIn version 3.1

: SEQ ID NO 60382

: LENGTH: 171

: TYPE: PRT

: ORGANISM: Zea mays subsp. mays

: FEATURE:

: NAME/KEY: misc\_feature

: LOCATION: 1..171

: OTHER INFORMATION: Xaa is any amino acid

: NAME/KEY: misc\_feature

: LOCATION: 1..171

: OTHER INFORMATION: Ceres Seq. ID 1947092

: US-09-708-427-60382

: Query Match

: Best Local Similarity 90.3%; Score 28; DB 5; Length 171;

: Matches 5; Conservative 1; Mismatches 0; Gaps 0;

: QY 1 plglxar 7

: Db 99 PLGISAR 105



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OM protein - protein search, using sw model

Run on: March 1, 2002, 06:47:48 ; Search time 12.55 Seconds  
(without alignments)  
12.552 Million cell updates/sec

Title: 09-876091-2  
Perfect score: 31  
Sequence: 1 plglxar 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Query Length	ID	Description
1	29	93.5	7	1 US-08-303-270-7	Sequence 7, Appl
2	29	93.5	7	3 US-08-950-618-14	Sequence 14, Appl
3	29	93.5	7	4 US-09-168-010-14	Sequence 14, Appl
4	29	93.5	7	4 US-09-144-419A-3	Sequence 3, Appl
5	28	90.3	8	3 US-07-961-307-2	Sequence 2, Appl
6	26	83.9	30	2 US-08-280-864A-10	Sequence 10, Appl
7	26	83.9	87	4 US-09-220-528-115	Sequence 115, Appl
8	26	83.9	237	4 US-09-220-528-32	Sequence 32, Appl
9	26	83.9	273	2 US-08-424-641B-9	Sequence 9, Appl
10	26	83.9	273	2 US-08-820-980-9	Sequence 9, Appl
11	26	83.9	273	2 US-08-826-439-9	Sequence 9, Appl
12	26	83.9	488	4 US-08-776-511-2	Sequence 2, Appl
13	26	83.9	508	2 US-08-850-293-5	Sequence 2, Appl
14	25	80.6	330	3 US-08-851-843A-203	Sequence 203, Appl
15	25	80.6	330	3 US-08-974-549A-322	Sequence 322, Appl
16	25	80.6	330	4 US-08-854-050-203	Sequence 203, Appl
17	25	80.6	408	2 US-08-926-258-2	Sequence 2, Appl
18	25	80.6	408	2 US-09-120-053-2	Sequence 2, Appl
19	25	80.6	408	4 US-09-198-312-2	Sequence 2, Appl
20	25	80.6	1141	1 US-08-363-300-2	Sequence 2, Appl
21	25	80.6	2259	4 US-09-413-814-70	Sequence 70, Appl
22	25	80.6	2439	3 US-09-335-409-7	Sequence 7, Appl
23	24	77.4	144	3 US-08-906-769-153	Sequence 153, Appl
24	24	77.4	144	3 US-08-906-616-153	Sequence 153, Appl
25	24	77.4	144	4 US-08-639-075A-153	Sequence 81, Appl
26	24	77.4	144	4 US-09-004-731-81	Sequence 153, Appl
27	24	77.4	144	4 US-09-012-431-153	Sequence 153, Appl

28	24	77.4	144	4	US-08-749-699-81	Sequence 81, Appl
29	24	77.4	144	4	US-09-012-692-153	Sequence 153, Appl
30	24	77.4	144	4	US-08-906-613-153	Sequence 153, Appl
31	24	77.4	149	3	US-08-834-224-4	Sequence 4, Appl
32	24	77.4	185	1	US-07-676-647-10	Sequence 10, Appl
33	24	77.4	185	1	US-08-449-329-10	Sequence 10, Appl
34	24	77.4	185	2	US-08-445-673-10	Sequence 10, Appl
35	24	77.4	185	2	US-08-585-258-10	Sequence 10, Appl
36	24	77.4	185	5	PCT-US91-03896-10	Sequence 10, Appl
37	24	77.4	192	4	US-08-444-818-165	Sequence 165, Appl
38	24	77.4	192	4	US-08-444-818-166	Sequence 166, Appl
39	24	77.4	192	4	US-08-444-818-167	Sequence 167, Appl
40	24	77.4	192	4	US-08-444-818-168	Sequence 168, Appl
41	24	77.4	192	4	US-08-444-818-169	Sequence 169, Appl
42	24	77.4	192	4	US-08-444-818-170	Sequence 170, Appl
43	24	77.4	233	4	US-09-004-731-27	Sequence 27, Appl
44	24	77.4	233	4	US-08-749-699-27	Sequence 27, Appl
45	24	77.4	250	1	US-08-378-761A-71	Sequence 71, Appl

#### ALIGNMENTS

RESULT 1  
US-08-303-270-7  
; Sequence 7, Application US/08303270  
; Patent No. 5646027  
; GENERAL INFORMATION:  
; APPLICANT: Ye, Qi-Zhuang  
; APPLICANT: Johnson, Linda L.  
; APPLICANT: Hupe, Donald J.  
; TITLE OF INVENTION: Process for the Production of  
; TITLE OF INVENTION: Gelatinase Catalytic Domain Protein  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Warner-Lambert Company  
; STREET: 2800 Plymouth Rd.  
; CITY: Ann Arbor  
; STATE: MI  
; COUNTRY: US  
; ZIP: 48105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/303,270  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Timney, Francis J.  
; REGISTRATION NUMBER: 33,069  
; REFERENCE/DOCKET NUMBER: 5120-FJT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 313 996-7295  
; TELEFAX: 313 996-1553  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-303-270-7

Query Match 93.5%; Score 29; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 plglxar 7  
|||||||

Db 1 PLGLXAR 7

RESULT 2

US-08-950-618-14

Sequence 14, Application US/08950618

Patent No. 6087325

GENERAL INFORMATION:

APPLICANT: The Liposome Company Inc.

APPLICANT: Pak, Charles

APPLICANT: Meers, Paul

APPLICANT: All, Shaikat

APPLICANT: Janoff, Andrew S.

APPLICANT: Franklin, J. Craig

APPLICANT: Erukulla, Ravi K.

TITLE OF INVENTION: Methods of liposomal Drug Delivery using

FILE REFERENCE: TLC 215A

CURRENT FILING DATE: 1997-10-15

EARLIER FILING DATE: 1996-10-15

NUMBER OF SEQ ID NOS: 44

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 14

LENGTH: 7

TYPE: PRT

ORGANISM: Peptides

FEATURE:

NAME/KEY: VARIANT

LOCATION: (5)...(5)

OTHER INFORMATION: N-3-(2,4-dinitrophenyl)-L-2,3-diaminoproplyl

FEATURE:

NAME/KEY: BINDING

LOCATION: (7)...(7)

OTHER INFORMATION: C-terminal amino group

US-08-950-618-14

Query Match

Best Local Similarity 93.5%; Score 29; DB 3; Length 7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 plglxar 7

Db 1 PLGLXAR 7

RESULT 3

US-09-168-010-14

Sequence 14, Application US/09168010A

Patent No. 6143716

GENERAL INFORMATION:

APPLICANT: The Liposome Company Inc.

APPLICANT: Pak, Charles

APPLICANT: Meers, Paul

APPLICANT: All, Shaikat

APPLICANT: Janoff, Andrew S.

APPLICANT: Franklin, J. Craig

APPLICANT: Erukulla, Ravi K.

TITLE OF INVENTION: Liposomal Peptide-Lipid Conjugates and

FILE REFERENCE: TLC 215B

CURRENT FILING DATE: 1998-10-07

EARLIER FILING DATE: 1996-10-15

NUMBER OF SEQ ID NOS: 44

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 14

LENGTH: 7

TYPE: PRT

ORGANISM: Peptides

FEATURE:

NAME/KEY: VARIANT

LOCATION: (5)...(5)

OTHER INFORMATION: N-3-(2,4-dinitrophenyl)-L-2,3-diaminoproplyl

FEATURE:

NAME/KEY: BINDING

LOCATION: (7)...(7)

OTHER INFORMATION: C-terminal amino group

US-09-168-010-14

Query Match

Best Local Similarity 93.5%; Score 29; DB 4; Length 7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 plglxar 7

Db 1 PLGLXAR 7

RESULT 4

US-09-144-419A-3

Sequence 3, Application US/09144419A

Patent No. 6187907

GENERAL INFORMATION:

APPLICANT: Chen, James

APPLICANT: Yeh, Li-An

TITLE OF INVENTION: TRIPLE HELIX COIL TEMPLATE HAVING A BIOLOGICALLY ACTIVE LIGAN

FILE REFERENCE: 08083/002001

CURRENT FILING DATE: 1998-08-31

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 7

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: VARIANT

LOCATION: (5)...(5)

OTHER INFORMATION: Xaa = N-3(2,4-dinitrophenyl)-L-2,3-diaminoproplyl

US-09-144-419A-3

Query Match

Best Local Similarity 93.5%; Score 29; DB 4; Length 7;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 plglxar 7

Db 1 PLGLXAR 7

RESULT 5

US-07-961-307-2

Sequence 2, Application US/07961307

Patent No. 6090785

GENERAL INFORMATION:

APPLICANT: Durelle, Philippe L.

APPLICANT: Esser, Craig K.

APPLICANT: Hagman, William K.

APPLICANT: Kopke, Ihor E.

TITLE OF INVENTION: Substituted N-Carboxyalkyl-peptidal

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESS: Merck & Co., Inc.

STREET: 126 E. Lincoln Avenue, P. O. Box 2000

CITY: Rahway

STATE: New Jersey

COUNTRY: USA

ZIP: 07065

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/961,307  
FILING DATE: 15-OCT-1992  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Rose, David L.  
REGISTRATION NUMBER: 26332  
REFERENCE/DOCKET NUMBER: 18829  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)594-4777  
TELEFAX: (908)594-4720  
TELEX: 138825  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-07-961-307-2

Query Match 90.3%; Score 28; DB 3; Length 8;  
Best Local Similarity 85.7%; Pred. No. 1.6e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 plglxar 7  
Db 2 PGLMAR 8

RESULT 6  
US-08-280-864A-10  
Sequence 10, Application US/08280864A  
Patent No. 5885574  
GENERAL INFORMATION:  
APPLICANT: Eliott, Steven G.  
TITLE OF INVENTION: Antibodies Which Activate an  
TITLE OF INVENTION: Erythropoietin Receptor  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 91320  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/280,864A  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-307  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-280-864A-10  
Query Match 83.9%; Score 26; DB 2; Length 30;  
Best Local Similarity 71.4%; Pred. No. 6.9;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 plglxar 7  
Db 3 PGLMAR 9

RESULT 7  
US-09-220-528-115  
Sequence 115, Application US/09220528A  
Patent No. 6284540  
GENERAL INFORMATION:  
APPLICANT: Mildrandt, Jeffrey D.  
TITLE OF INVENTION: Artemin, A No. 6284540el Neutrotrophic Factor  
FILE REFERENCE: 6029-7998  
CURRENT APPLICATION NUMBER: US/09/220,528A  
CURRENT FILING DATE: 1998-12-24  
EARLIER APPLICATION NUMBER: 09/218,698  
EARLIER FILING DATE: 1998-12-22  
EARLIER APPLICATION NUMBER: 60/108,148  
EARLIER FILING DATE: 1998-11-12  
EARLIER APPLICATION NUMBER: 09/163,283  
EARLIER FILING DATE: 1998-09-29  
NUMBER OF SEQ ID NOS: 120  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 115  
LENGTH: 87  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-220-528-115

Query Match 83.9%; Score 26; DB 4; Length 87;  
Best Local Similarity 71.4%; Pred. No. 22;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 plglxar 7  
Db 33 PGLMAR 39

RESULT 8  
US-09-220-528-32  
Sequence 32, Application US/09220528A  
Patent No. 6284540  
GENERAL INFORMATION:  
APPLICANT: Mildrandt, Jeffrey D.  
TITLE OF INVENTION: Artemin, A No. 6284540el Neutrotrophic Factor  
FILE REFERENCE: 6029-7998  
CURRENT APPLICATION NUMBER: US/09/220,528A  
CURRENT FILING DATE: 1998-12-24  
EARLIER APPLICATION NUMBER: 09/218,698  
EARLIER FILING DATE: 1998-12-22  
EARLIER APPLICATION NUMBER: 60/108,148  
EARLIER FILING DATE: 1998-11-12  
EARLIER APPLICATION NUMBER: 09/163,283  
EARLIER FILING DATE: 1998-09-29  
NUMBER OF SEQ ID NOS: 120  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 32  
LENGTH: 237  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-220-528-32

Query Match 83.9%; Score 26; DB 4; Length 237;  
Best Local Similarity 71.4%; Pred. No. 68;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglxar 7  
1111 :1  
DB 31 PLGLSNO 37

## RESULT 9

US-08-424-641B-9  
; Sequence 9, Application US/08424641B  
; Patent No. 5824523  
; GENERAL INFORMATION:  
; APPLICANT: Sylvain Moineau, Shirley A.  
; APPLICANT: Walker, Ebenezer R. Vedamuthu,  
; APPLICANT: and Peter A. Vandenberg  
; TITLE OF INVENTION: Isolated DNA Encoding  
; TITLE OF INVENTION: Enzyme For Phage  
; TITLE OF INVENTION: Resistance  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ian C. McLeod  
; STREET: 2190 Commons Parkway  
; CITY: Okemos  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 48864  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
; MEDIUM TYPE: storage  
; COMPUTER: Acer  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424, 641B  
; FILING DATE: April 19, 1995  
; CLASSIFICATION: 435  
; INFORMATION FOR SEQ ID NO: 9:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/366, 480  
; FILING DATE: December 30, 1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ian C. McLeod  
; REGISTRATION NUMBER: 20, 931  
; REFERENCE/DOCKET NUMBER: MT 4.1-151  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (517) 347-4100  
; TELEFAX: (517) 347-4103  
; TELEX: NO. 5824523e  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 273 Amino Acids  
; TYPE: Amino Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Peptide  
US-08-424-641B-9

Query Match 83.9%; Score 26; DB 2; Length 273;  
Best Local Similarity 71.4%; Pred. No. 80;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglxar 7  
1111 :1  
DB 195 PLGLLSR 201

RESULT 10  
US-08-820-980-9  
; Sequence 9, Application US/08820980  
; Patent No. 5925388

; GENERAL INFORMATION:  
; APPLICANT: Sylvain Moineau, Shirley A.  
; APPLICANT: Walker, Ebenezer R. Vedamuthu,  
; APPLICANT: and Peter A. Vandenberg  
; TITLE OF INVENTION: Isolated DNA Encoding  
; TITLE OF INVENTION: Enzyme For Phage  
; TITLE OF INVENTION: Resistance  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ian C. McLeod  
; STREET: 2190 Commons Parkway  
; CITY: Okemos  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 48864  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb  
; MEDIUM TYPE: storage  
; COMPUTER: Acer  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/820, 980  
; FILING DATE:  
; CLASSIFICATION: 435  
; INFORMATION FOR SEQ ID NO: 9:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/424, 641  
; FILING DATE: April 19, 1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ian C. McLeod  
; REGISTRATION NUMBER: 20, 931  
; REFERENCE/DOCKET NUMBER: Quest 4.1-156  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (517) 347-4100  
; TELEFAX: (517) 347-4103  
; TELEX: NO. 5925388e  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 273 Amino Acids  
; TYPE: Amino Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; MOLECULE TYPE: Peptide  
US-08-820-980-9

Query Match 83.9%; Score 26; DB 2; Length 273;  
Best Local Similarity 71.4%; Pred. No. 80;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 plglxar 7  
1111 :1  
DB 195 PLGLLSR 201

RESULT 11  
US-08-826-439-9  
; Sequence 9, Application US/08826439  
; Patent No. 5972673  
; GENERAL INFORMATION:  
; APPLICANT: Sylvain Moineau, Shirley A.  
; APPLICANT: Walker, Ebenezer R. Vedamuthu,  
; APPLICANT: and Peter A. Vandenberg  
; TITLE OF INVENTION: Isolated DNA Encoding  
; TITLE OF INVENTION: Enzyme For Phage  
; TITLE OF INVENTION: Resistance  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ian C. McLeod  
; STREET: 2190 Commons Parkway  
; CITY: Okemos  
; STATE: Michigan

COUNTRY: USA  
ZIP: 48864  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 KB  
MEDIUM TYPE: Storage  
COMPUTER: Acer  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/826,439  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/424,641  
FILING DATE: April 19, 1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Ian C. McLeod  
REGISTRATION NUMBER: 20,931  
REFERENCE/DOCKET NUMBER: Quest 4.1-155  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (517) 347-4100  
TELEFAX: (517) 347-4103  
TELEX: No. 5972673e  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 273 Amino Acids  
TYPE: Amino Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
MOLECULE TYPE: Peptide  
US-08-826-439-9

Query Match 83.9% Score 26; DB 2; Length 273;  
Best Local Similarity 71.4%; Pred. No. 80;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 pliglar 7  
111111  
Db 195 PGLLSR 201

RESULT 12  
US-08-776-511-2  
Sequence 2, Application US/08776511  
Patent No. 6153190  
GENERAL INFORMATION:  
APPLICANT: Young, Peter R.  
APPLICANT: Erickson-Miller, Connie  
TITLE OF INVENTION: Method for Obtaining Receptor Agonist  
TITLE OF INVENTION: Antibodies  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Smithline Beecham Corporation- Corporate  
ADDRESSEE: Patents  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406-2799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/776,511  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Jarvis, Herbert H.  
REGISTRATION NUMBER: 31,171

REFERENCE/DOCKET NUMBER: SEC P50349-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-5015  
TELEFAX: 610-270-5090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 488 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-776-511-2

Query Match 83.9% Score 26; DB 4; Length 488;  
Best Local Similarity 71.4%; Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 pliglar 7  
111111  
Db 148 PVLGLAR 154

RESULT 13  
US-08-850-293-5  
Sequence 5, Application US/08850293  
Patent No. 5843726  
GENERAL INFORMATION:  
APPLICANT: Lee, Jong Y.  
TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR  
TITLE OF INVENTION: PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C., P.A.  
STREET: 60 South Sixth Street, Suite 3300  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Fastseq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/850,293  
FILING DATE: 05-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/499,643  
FILING DATE: 07-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/106,815  
FILING DATE: 16-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Ellinger, Mark S.  
REGISTRATION NUMBER: 34,812  
REFERENCE/DOCKET NUMBER: 07004/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612/335-5070  
TELEFAX: 612/288-9696  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 508 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-850-293-5

Query Match 83.9% Score 26; DB 2; Length 508;  
Best Local Similarity 71.4%; Pred. No. 1.6e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 plglxar 7  
1:1111  
Db 148 pvglvlar 154

RESULT 14  
US-08-851-843A-203  
; Sequence 203, Application US/08851843A  
; Patent No. 6093809  
; GENERAL INFORMATION:  
; APPLICANT: Cecch, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: No. 6093809el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/851,843A  
; FILING DATE: 06-MAY-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002930US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 203:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 330 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-851-843A-203

Query Match 80.6%, Score 25; DB 3; Length 330;  
Best Local Similarity 71.4%; Pred. No. 1.7e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 plglxar 7  
111111  
Db 270 pvglvlar 276

RESULT 15  
US-08-974-549A-322  
; Sequence 322, Application US/08974549A  
; Patent No. 6166178  
; GENERAL INFORMATION:  
; APPLICANT: Cecch, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin B.  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,549A  
; FILING DATE: 19-NOV-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/844,419  
; FILING DATE: 18-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/846,017  
; FILING DATE: 25-APR-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/851,843  
; FILING DATE: 06-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/854,050  
; FILING DATE: 09-MAY-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/911,312  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/912,951  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/915,503  
; FILING DATE: 14-AUG-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/17618  
; FILING DATE: 01-OCT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US97/17885  
; FILING DATE: 01-OCT-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph Ted  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 015389-002610US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 322:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 330 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear



; MOLECULE TYPE: peptide  
US-08-974-549A-322

Query Match 80.6%; Score 25; DB 4; Length 330;  
Best Local Similarity 71.4%; Pred. No. 1.7e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 plglxar 7  
11111  
1;  
Db 270 PLGLQAQ 276

Search completed: March 1, 2002, 06:48:29  
Job time: 41 sec

